

71

MSKPP-----APNPTPPH-----LSRTFTIG-----GMSFEVADG
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 Consensus

72 I II III IV 142
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 Consensus

143 V VI VII 213
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 Consensus

214 VII VIII IX 264
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 Consensus

265 X 355
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 Consensus

356 XI 426
 MCKK3 MCKK4 MCKK1 MCKK2 PBS2
 Consensus

FIG. 1

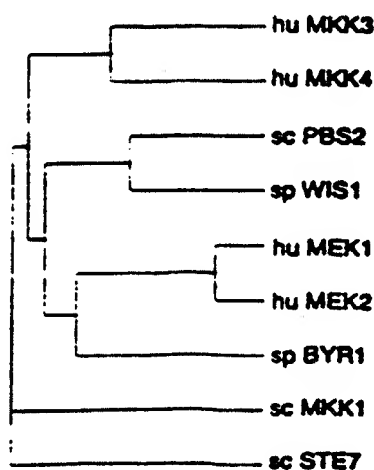


FIG. 2

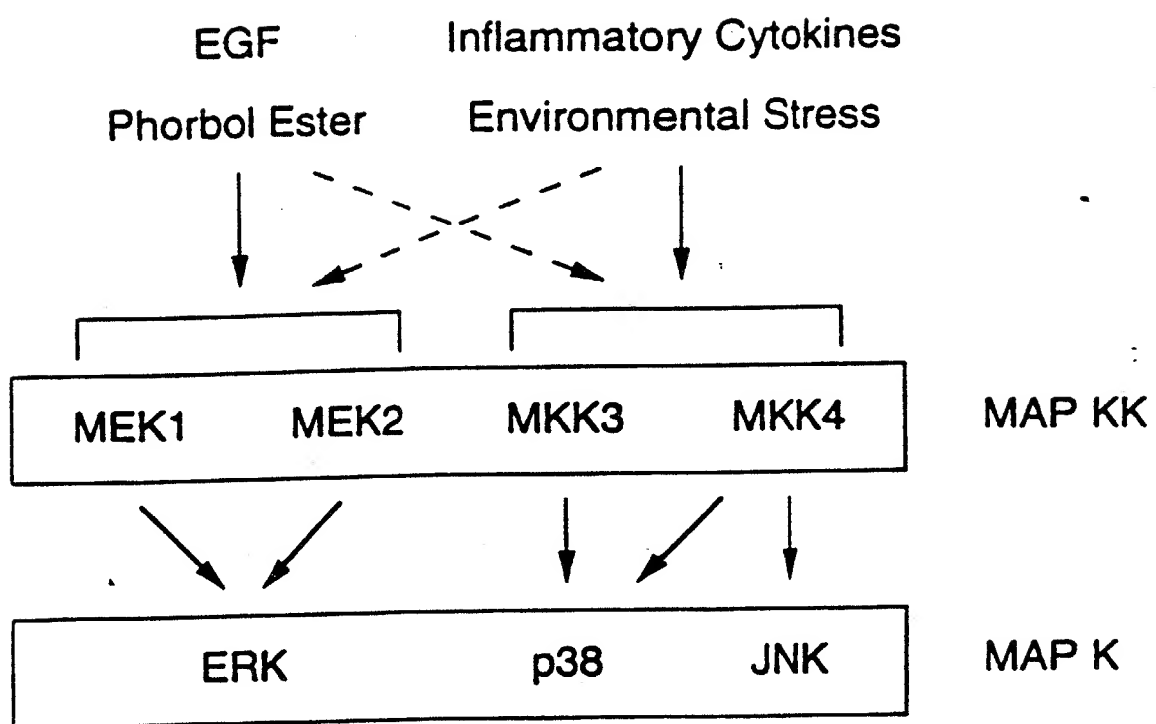


FIG. 3

FIG. 4

5	10	15	20	25	30	35	40	45	50	55	60								
	*		*		*		*		*		*								
TGGCTGGCAA	TGGCCTTGCT	GACCTCGAGC	CGGGCCACG	TGGGGACCTT	TGGAGCACAG	ACCGACCGTT	ACCGGAACGA	CTGGAGCTCG	GCCCAGGTGC	ACCCCTGGAA	ACCTCGTGTC								
65	70	75	80	85	90	95	100	105	110	115	120								
	*		*		*		*		*		*								
CCTACGATCC	TGGTGCAAGG	CCGGTGGATG	CAGAGGCCAG	TCCATATACC	ACCCAGGCCT	GGATGCTAGG	ACCACGTTCC	GGCCACCTAC	GTCTCCGGTC	AGGTATATGG	TGGGTCCGGA								
125	130	135	140	145	150	155	160	165	170	175	180								
	*		*		*		*		*		*								
GCGAGGAGCG	TGGTCCCCAC	CCATCCAGCC	CATATGTGCA	AGTGGCCCTTG	ACAGAGAGGC	GGCTCCTCGC	ACCAGGGGTG	GGTAGGTCGG	GTATACACGT	TCACGGGAAC	TGTCTCTCCG								
185	190	195	200	205	210	215	220	225	230	235	240								
	*		*		*		*		*		*								
TGGTCATATC	CATGGTGACC	ATTTATGGGC	CACAACAGGT	CCCCATCTGC	GCAGTGAACC	ACCACTATAG	GTACCACTGG	TAAATACCGG	GTGTTGTCCA	GGGGTAGACG	CGTCACTTGG								
245	250	255	260	265	270	275	280	285	290	295	300								
	*		*		*		*		*		*								
CTGTGCTGAG	CACCTTGCAG	ACGTGATCTT	GCTTCGTCCT	GCAGCACTGT	GCGGGGCAGG	GACACGACTC	GTGGAACGTC	TGCACTAGAA	CGAAGCAGGA	CGTCGTGACA	CGCCCCGTCC								
305	310	315	320	325	330	335	340	345	350	355									
	*		*		*		*		*										
AAAATCCAAG	AGGAAGAAGG	ATCTACGGAT	ATCCTGCG	ATG	TCC	AAG	CCA	CCC	GCA	TTTtaggttc	TCCTTCTTCC	TAGATGCCTA	TAGGACG	TAC	AGG	TTC	GGT	GGG	CGT
										Met	Ser	Lys	Pro	Pro	Ala>				
360	365	370	375	380	385	390	395	400											
	*		*		*		*		*										
CCC AAC CCC ACA CCC CCC CGG AAC CTG GAC TCC CGG ACC TTC ATC ACC	GGG TTG GGG TGT GGG GGG GCC TTG GAC CTG AGG GCC TGG AAG TAG TGG	Pro Asn Pro Thr Pro Pro Arg Asn Leu Asp Ser Arg Thr Phe Ile Thr>																	
405	410	415	420	425	430	435	440	445	450										
	*		*		*		*		*										
ATT GGA GAC AGA AAC TTT GAG GTG GAG GCT GAT GAC TTG GTG ACC ATC	TAA CCT CTG TCT TTG AAA CTC CAC CTC CGA CTA CTG AAC CAC TAG TGG TAG	Ile Gly Asp Arg Asn Phe Glu Val Glu Ala Asp Asp Leu Val Thr Ile>																	
455	460	465	470	475	480	485	490	495											
	*		*		*		*		*										
TCA GAA CTG GGC CGT GGA GCC TAT GGG GTG GTA GAG AAG GTG CGG CAC	AGT CTT GAC CCG GCA CCT CGG ATA CCC CAC CAT CTC TTC CAC GCC GTG	Ser Glu Leu Gly Arg Gly Ala Tyr Gly Val Val Glu Lys Val Arg His>																	
500	505	510	515	520	525	530	535	540	545										
	*		*		*		*		*										
GCC CAG AGC GGC ACC ATC ATG GCC GTG AAG CGG ATC CGG GCC ACC GTG	CGG GTC TCG CCG TGG TAG TAC CGG CAC TTC GCC TAG GCC CGG TGG CAC	Ala Gln Ser Gly Thr Ile Met Ala Val Lys Arg Ile Arg Ala Thr Val>																	
550	555	560	565	570	575	580	585	590	595										
	*		*		*		*		*										
AAC TCA CAG GAG CAG AAG CGG CTG CTC ATG GAC CTG GAC ATC AAC ATG	TTG AGT GTC CTC GTC TTC GCC GAC GAG TAC CTG GAC CTG TAG TTG TAC	Asn Ser Gln Glu Gln Lys Arg Leu Leu Met Asp Leu Asp Ile Asn Met>																	

FIG. 4 - CONT'D

600	605	610	615	620	625	630	635	640							
*		*		*		*		*							
CGC	ACG	GTC	GAC	TGT	TTC	TAC	ACT	GTC	ACC	TTC	TAC	GGG	GCA	CTA	TTC
GCG	TGC	CAG	CTG	ACA	AAG	ATG	TGA	CAG	TGG	AAG	ATG	CCC	CGT	GAT	AAG
Arg	Thr	Val	Asp	Cys	Phe	Tyr	Thr	Val	Thr	Phe	Tyr	Gly	Ala	Leu	Phe>
645	650	655	660	665	670	675	680	685	690						
	*		*		*		*		*						
AGA	GAG	GGA	GAC	GTG	TGG	ATC	TGC	ATG	GAG	CTC	ATG	GAC	ACA	TCC	TTG
TCT	CTC	CCT	CTG	CAC	ACC	TAG	ACG	TAC	CTC	GAG	TAC	CTG	TGT	AGG	AAC
Arg	Glu	Gly	Asp	Val	Trp	Ile	Cys	Met	Glu	Leu	Met	Asp	Thr	Ser	Leu>
695	700	705	710	715	720	725	730	735							
	*		*		*		*		*						
GAC	AAG	TTC	TAC	CGG	AAG	GTG	CTG	GAT	AAA	AAC	ATG	ACA	ATT	CCA	GAG
CTG	TTC	AAG	ATG	GCC	TTC	CAC	GAC	CTA	TTT	TTG	TAC	TGT	TAA	GGT	CTC
Asp	Lys	Phe	Tyr	Arg	Lys	Val	Leu	Asp	Lys	Asn	Met	Thr	Ile	Pro	Glu>
740	745	750	755	760	765	770	775	780	785						
*		*		*		*		*							
GAC	ATC	CTT	GGG	GAG	ATT	GCT	GTG	TCT	ATC	GTG	CGG	GCC	CTG	GAG	CAT
CTG	TAG	GAA	CCC	CTC	TAA	CGA	CAC	AGA	TAG	CAC	GCC	CGG	GAC	CTC	GTA
Asp	Ile	Leu	Gly	Glu	Ile	Ala	Val	Ser	Ile	Val	Arg	Ala	Leu	Glu	His>
790	795	800	805	810	815	820	825	830	835						
*		*		*		*		*							
CTG	CAC	AGC	AAG	CTG	TCG	GTG	ATC	CAC	AGA	GAT	GTG	AAG	CCC	TCC	AAT
GAC	GTG	TCG	TTC	GAC	AGC	CAC	TAG	GTG	TCT	CTA	CAC	TTC	GGG	AGG	TTA
Leu	His	Ser	Lys	Leu	Ser	Val	Ile	His	Arg	Asp	Val	Lys	Pro	Ser	Asn>
840	845	850	855	860	865	870	875	880							
*		*		*		*		*							
GTC	CTT	ATC	AAC	AAG	GAG	GGC	CAT	GTG	AAG	ATG	TGT	GAC	TTT	GGC	ATC
CAG	GAA	TAG	TTG	TTC	CTC	CCG	GTA	CAC	TTC	TAC	ACA	CTG	AAA	CCG	TAG
Val	Leu	Ile	Asn	Lys	Glu	Gly	His	Val	Lys	Met	Cys	Asp	Phe	Gly	Ile>
885	890	895	900	905	910	915	920	925	930						
	*		*		*		*		*						
AGT	GGC	TAC	TTG	GTG	GAC	TCT	GTG	GCC	AAG	ACG	ATG	GAT	GCC	GGC	TGC
TCA	CCG	ATG	AAC	CAC	CTG	AGA	CAC	CGG	TTC	TGC	TAC	CTA	CGG	CCG	ACG
Ser	Gly	Tyr	Leu	Val	Asp	Ser	Val	Ala	Lys	Thr	Met	Asp	Ala	Gly	Cys>
935	940	945	950	955	960	965	970	975							
	*		*		*		*		*						
AAG	CCC	TAC	ATG	GCC	CCT	GAG	AGG	ATC	AAC	CCA	GAG	CTG	AAC	CAG	AAG
TTC	GGG	ATG	TAC	CGG	GGA	CTC	TCC	TAG	TTG	GGT	CTC	GAC	TTG	GTC	TTC
Lys	Pro	Tyr	Met	Ala	Pro	Glu	Arg	Ile	Asn	Pro	Glu	Leu	Asn	Gln	Lys>
980	985	990	995	1000	1005	1010	1015	1020	1025						
*		*		*		*		*							
GGC	TAC	AAT	GTC	AAG	TCC	GAC	GTG	TGG	AGC	CTG	GGC	ATC	ACC	ATG	ATT
CCG	ATG	TTA	CAG	TTC	AGG	CTG	CAG	ACC	TCG	GAC	CCG	TAG	TGG	TAC	TAA
Gly	Tyr	Asn	Val	Lys	Ser	Asp	Val	Trp	Ser	Leu	Gly	Ile	Thr	Met	Ile>
1030	1035	1040	1045	1050	1055	1060	1065	1070	1075						
*		*		*		*		*							
GAG	ATG	GCC	ATC	CTG	CGG	TTC	CCT	TAC	GAG	TCC	TGG	GGG	ACC	CCG	TTC
CTC	TAC	CGG	TAG	GAC	GCC	AAG	GGA	ATG	CTC	AGG	ACC	CCC	TGG	GGC	AAG
Glu	Met	Ala	Ile	Leu	Arg	Phe	Pro	Tyr	Glu	Ser	Trp	Gly	Thr	Pro	Phe>
1080	1085	1090	1095	1100	1105	1110	1115	1120							

FIG. 4 - CONT'D

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      *           *           *           *           *
CAG CAG CTG AAG CAG GTG GTG GAG GAG CCG TCC CCC CAG CTC CCA GCC
GTC GTC GAC TTC GTC CAC CAC CTC CTC GGC AGG GGG GTC GAG GGT CCG
Gln Gln Leu Lys Gln Val Val Glu Glu Pro Ser Pro Gln Leu Pro Ala>

1125   1130   1135   1140   1145   1150   1155   1160   1165   1170
      *           *           *           *           *
GAC CGT TTC TCC CCC GAG TTT GTG GAC TTC ACT GCT CAG TGC CTG AGG
CTG GCA AAG AGG GGG CTC AAA CAC CTG AAG TGA CGA GTC ACG GAC TCC
Asp Arg Phe Ser Pro Glu Phe Val Asp Phe Thr Ala Gln Cys Leu Arg>

1175   1180   1185   1190   1195   1200   1205   1210   1215
      *           *           *           *           *
AAG AAC CCC GCA GAG CGT ATG AGC TAC CTG GAG CTG ATG GAG CAC CCC
TTC TTG GGG CGT CTC GCA TAC TCG ATG GAC CTC GAC TAC CTC GTG GGG
Lys Asn Pro Ala Glu Arg Met Ser Tyr Leu Glu Leu Met Glu His Pro>

1220   1225   1230   1235   1240   1245   1250   1255   1260   1265
      *           *           *           *           *
TTC TTC ACC TTG CAC AAA ACC AAG AAG ACG GAC ATT GCT GCC TTC GTG
AAG AAG TGG AAC GTG TTT TGG TTC TTC TGC CTG TAA CGA CGG AAG CAC
Phe Phe Thr Leu His Lys Thr Lys Lys Thr Asp Ile Ala Ala Phe Val>

1270   1275   1280   1285   1290   1295   1300   1305   1310   1315   1320
      *           *           *           *           *
AAG AAG ATC CTG GGA GAA GAC TCA TAGGGGCTG GGCCTCGGAC CCCACTCCGG
TTC TTC TAG GAC CCT CTT CTG AGT ATCCCCGAC CCGGAGCCTG GGGTGAGGCC
Lys Lys Ile Leu Gly Glu Asp Ser> (SEQ ID NO:2)

1325   1330   1335   1340   1345   1350   1355   1360   1365   1370   1375   1380
      *           *           *           *           *
CCCTCCAGAG CCCACAGCC CCATCTGCGG GGGCAGTGCT CACCCACACC ATAAGCTACT
GGGAGGTCTC GGGGTGTCGG GGTAGACGCC CCCGTCACGA GTGGGTGTGG TATTCGATGA

1385   1390   1395   1400   1405   1410   1415   1420   1425   1430   1435   1440
      *           *           *           *           *
GCCATCCTGG CCCAGGGCAT CTGGGAGGAA CCGAGGGGGC TGCTCCCACC TGGCTCTGTG
CGGTAGGACC GGGTCCCGTA GACCCCTCCTT GGCTCCCCCG ACGAGGGTGG ACCGAGACAC

1445   1450   1455   1460   1465   1470   1475   1480   1485   1490   1495   1500
      *           *           *           *           *
GCGAGCCATT TGTCCCAAGT GCCAAAGAAG CAGACCATTG GGGCTCCCAG CCAGGCCCTT
CGCTCGGTAA ACAGGGTTCA CGGTTTCTTC GTCTGGTAAC CCCGAGGGTC GGTCCGGGAA

1505   1510   1515   1520   1525   1530   1535   1540   1545   1550   1555   1560
      *           *           *           *           *
GTCCGCCCCA CCAGTGCCTC TCCCTGCTGC TCCTAGGACC CGTCTCCAGC TGCTGAGATC
CAGCCGGGGT GGTACGGGAG AGGGACGACG AGGATCCTGG GCAGAGGTCTG ACCACTCTAG

1565   1570   1575   1580   1585   1590   1595   1600   1605   1610   1615   1620
      *           *           *           *           *
CTGGACTGAG GGGGCCTGGA TGCCCCCTGT GGATGCTGCT GCCCCCTGCAC AGCAGGCTGC
GACCTGACTC CCCCAGACCT ACGGGGGACA CCTACGACGA CGGGGACGTG TCGTCCGACG

1625   1630   1635   1640   1645   1650   1655   1660   1665   1670   1675   1680
      *           *           *           *           *
CAGTGCCTGG GTGGATGGGC CACCGCCTTG CCCAGCCTGG ATGCCATCCA AGTTGTATAT
GTCACGGACC CACCTACCCG GTGGCGGAAC GGGTCGGACC TACGGTAGGT TCAACATATA

1685   1690   1695   1700   1705   1710   1715   1720   1725   1730   1735   1740
      *           *           *           *           *
TTTTTTAATC TCTCGACTGA ATGGACTTTG CACACTTTGG CCCAGGGTGG CCACACCTCT

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FIG..4 - CONT'D

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AAAAAATTAG AGAGCTGACT TACCTGAAAC GTGTGAAACC GGTCCCACC GGTGTGGAGA
 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800
      *      *      *      *      *      *      *      *
ATCCCGGCTT TGGTGCGGGG TACACAAGAG GGGATGAGTT GTGTGAATAC CCCAAGACTC
TAGGGCCGAA ACCACGCCCC ATGTGTTCTC CCCTACTCAA CACACTTATG GGGTTCTGAG

 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860
      *      *      *      *      *      *      *      *
CCATGAGGGA GATGCCATGA GCCGCCCAAG GCCTTCCCCCT GGCAGTGGCA AACAGGGCCT
GGTACTCCCT CTACGGTACT CGGCGGGTTC CGGAAGGGGA CCGTGACCGT TTGTCCCGGA

 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920
      *      *      *      *      *      *      *      *
CTGCGGAGCA CACTGGCTCA CCCAGTCCTG CCCGCCACCG TTATCGGTGT CATTACCTT
GACGCCTCGT GTGACCGAGT GGGTCAGGAC GGGCGGTGGC AATAGCCACA GTAAGTGGAA

 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980
      *      *      *      *      *      *      *      *
TCGTGTTTTT TTTAATTTAT CCTCTGTTGA TTTTTCTTTT TGCTTTATGG GTTTGGCTTG
AGCACAAAAA AAATTAAATA GGAGACAACT AAAAAAGAAA ACGAAATACC CAAACCGAAC

 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030
      *      *      *      *      *      *      *      *
TTTTTCTTGC ATGGTTTGGA GCTGATCGCT TCTCCCCCAC CCCCTAGGGG (SEQ ID NO: 1)
AAAAAGAACG TACCAAACCT CGACTAGCGA AGAGGGGGTG GGGGATCCCC

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FIG. 5

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      5    10    15    20    25    30    35    40    45    50    55    60
      *      *      *      *      *      *      *      *      *      *
TAGCTGCAGC ACAGCCTTCC CTAACGTTGC AACTGGGGGA AAAATCACTT TCCAGTCTGT
ATCGACGTCG TGTCGGAAGG GATTGCAACG TTGACCCCTT TTTTAGTGAA AGGTCAGACA

      65    70    75    80    85    90    95   100   105   110   115   120
      *      *      *      *      *      *      *      *      *      *
TTTGCAAGGT GTGCATTTCC ATCTTGATTG CCTGAAAGTC CATCTGCTGC ATCGGTCAAG
AAACGTTCCA CACGTAAAGG TAGAACTAAG GGACTTTTCAG GTAGACGACG TAGCCAGTTC

      125   130   135   140   145   150   155   160   165   170   175   180
      *      *      *      *      *      *      *      *      *      *
AGAAACTCCA CTTCATGAA GATTGCACGC CTGCAGCTTG CATCTTTGTT GCAAAACTAG
TCTTTGAGGT GAACGTACTT CTAACGTGCG GACGTGGAAC GTAGAAACAA CGTTTTGATC

      185   190   195   200   205   210   215   220   225   230   235   240
      *      *      *      *      *      *      *      *      *      *
CTACAGAAGA GAAGCAAGGC AAAGTCTTTT GTGCTCCCCT CCCCCATCAA AGGAAAGGGG
GATGTCTTCT CTTCGTTCCG TTTCAGAAAA CACGAGGGGA GGGGGTAGTT TCCTTTCCCC

      245   250   255   260   265   270   275   280   285
      *      *      *      *      *      *      *      *
AAA ATG TCT CAG TCG AAA GGC AAG AAG CGA AAC CCT GGC CTT AAA ATT
TTT TAC AGA GTC AGC TTT CCG TTC TTC GCT TTG GGA CCG GAA TTT TAA
Met Ser Gln Ser Lys Gly Lys Lys Arg Asn Pro Gly Leu Lys Ile>

290   295   300   305   310   315   320   325   330   335
*      *      *      *      *      *      *      *
CCA AAA GAA GCA TTT GAA CAA CCT CAG ACC AGT TCC ACA CCA CCT AGA
GGT TTT CTT CGT AAA CTT GTT GGA GTC TGG TCA AGG TGT GGT GGA TCT
Pro Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg>

340   345   350   355   360   365   370   375   380
*      *      *      *      *      *      *      *
GAT TTA GAC TCC AAG GCT TGC ATT TCT ATT GGA AAT CAG AAC TTT GAG
CTA AAT CTG AGG TTC CGA ACG TAA AGA TAA CCT TTA GTC TTG AAA CTC
Asp Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu>

385   390   395   400   405   410   415   420   425   430
*      *      *      *      *      *      *      *
GTG AAG GCA GAT GAC CTG GAG CCT ATA ATG GAA CTG GGA CGA GGT GCG
CAC TTC CGT CTA CTG GAC CTC GGA TAT TAC CTT GAC CCT GCT CCA CGC
Val Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala>

435   440   445   450   455   460   465   470   475   480
*      *      *      *      *      *      *      *
TAC GGG GTG GTG GAG AAG ATG CGG CAC GTG CCC AGC GGG CAG ATC ATG
ATG CCC CAC CAC CTC TTC TAC GCC GTG CAC GGG TCG CCC GTC TAG TAC
Tyr Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met>

485   490   495   500   505   510   515   520   525
*      *      *      *      *      *      *      *
GCA GTG AAG CGG ATC CGA GCC ACA GTA AAT AGC CAG GAA CAG AAA CGG
CGT CAC TTC GCC TAG GCT CGG TGT CAT TTA TCG GTC CTT GTC TTT GCC
Ala Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg>

530   535   540   545   550   555   560   565   570   575
*      *      *      *      *      *      *      *
CTA CTG ATG GAT TTG GAT ATT TCC ATG AGG ACG GTG GAC TGT CCA TTC
GAT GAC TAC CTA AAC CTA TAA AGG TAC TCC TGC CAC CTG ACA GGT AAG

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FIG. 5 - CONT'D

Leu Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe>
 580 585 590 595 600 605 610 615 620
 * * * * *
 ACT GTC ACC TTT TAT GGC GCA CTG TTT CGG GAG GGT GAT GTG TGG ATC
 TGA CAG TGG AAA ATA CCG CGT GAC AAA GCC CTC CCA CTA CAC ACC TAG
 Thr Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile>
 625 630 635 640 645 650 655 660 665 670
 * * * * *
 TGC ATG GAG CTC ATG GAT ACA TCA CTA GAT AAA TTC TAC AAA CAA GTT
 ACG TAC CTC GAG TAC CTA TGT AGT GAT CTA TTT AAG ATG TTT GTT CAA
 Cys Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val>
 675 680 685 690 695 700 705 710 715 720
 * * * * *
 ATT GAT AAA GGC CAG ACA ATT CCA GAG GAC ATC TTA GGG AAA ATA GCA
 TAA CTA TTT CCG GTC TGT TAA GGT CTC CTG TAG AAT CCC TTT TAT CGT
 Ile Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala>
 725 730 735 740 745 750 755 760 765
 * * * * *
 GTT TCT ATT GTA AAA GCA TTA GAA CAT TTA CAT AGT AAG CTG TCT GTC
 CAA AGA TAA CAT TTT CGT AAT CTT GTA AAT GTA TCA TTC GAC AGA CAG
 Val Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val>
 770 775 780 785 790 795 800 805 810 815
 * * * * *
 ATT CAC AGA GAC GTC AAG CCT TCT AAT GTA CTC ATC AAT GCT CTC GGT
 TAA GTG TCT CTG CAG TTC GGA AGA TTA CAT GAG TAG TTA CGA GAG CCA
 Ile His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly>
 820 825 830 835 840 845 850 855 860
 * * * * *
 CAA GTG AAG ATG TGC GAT TTT GGA ATC AGT GGC TAC TTG GTG GAC TCT
 GTT CAC TTC TAC ACG CTA AAA CCT TAG TCA CCG ATG AAC CAC CTG AGA
 Gln Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser>
 865 870 875 880 885 890 895 900 905 910
 * * * * *
 GTT GCT AAA ACA ATT GAT GCA GGT TGC AAA CCA TAC ATG GCC CCT GAA
 CAA CGA TTT TGT TAA CTA CGT CCA ACG TTT GGT ATG TAC CGG GGA CTT
 Val Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu>
 915 920 925 930 935 940 945 950 955 960
 * * * * *
 AGA ATA AAC CCA GAG CTC AAC CAG AAG GGA TAC AGT GTG AAG TCT GAC
 TCT TAT TTG GGT CTC GAG TTG GTC TTC CCT ATG TCA CAC TTC AGA CTG
 Arg Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp>
 965 970 975 980 985 990 995 1000 1005
 * * * * *
 ATT TGG AGT CTG GGC ATC ACG ATG ATT GAG TTG GCC ATC CTT CGA TTT
 TAA ACC TCA GAC CCG TAG TGC TAC TAA CTC AAC CGG TAG GAA GCT AAA
 Ile Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe>
 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055
 * * * * *
 CCC TAT GAT TCA TGG GGA ACT CCA TTT CAG CAG CTC AAA CAG GTG GTA
 GGG ATA CTA AGT ACC CCT TGA GGT AAA GTC GTC GAG TTT GTC CAC CAT
 Pro Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val>

FIG. 5 - CONT'D

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1060 1065 1070 1075 1080 1085 1090 1095 1100
*      *      *      *      *      *      *      *
GAG GAG CCA TCG CCA CAA CTC CCA GCA GAC AAG TTC TCT GCA GAG TTT
CTC CTC GGT AGC GGT GTT GAG GGT CGT CTG TTC AAG AGA CGT CTC AAA
Glu Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe>

1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
*      *      *      *      *      *      *      *
GTT GAC TTT ACC TCA CAG TGC TTA AAG AAG AAT TCC AAA GAA CGG CCT
CAA CTG AAA TGG AGT GTC ACG AAT TTC TTC TTA AGG TTT CTT GCC GGA
Val Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro>

1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
*      *      *      *      *      *      *      *
ACA TAC CCA GAG CTA ATG CAA CAT CCA TTT TTC ACC CTA CAT GAA TCC
TGT ATG GGT CTC GAT TAC GTT GTA GGT AAA AAG TGG GAT GTA CTT AGG
Thr Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser>

1205 1210 1215 1220 1225 1230 1235 1240 1245 1250
*      *      *      *      *      *      *      *
AAA GGA ACA GAT GTG GCA TCT TTT GTA AAA CTG ATT CTT GGA GAC TAAAA
TTT CCT TGT CTA CAC CGT AGA AAA CAT TTT GAC TAA GAA CCT CTG ATTTT
Lys Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp> (SEQ ID NO:4)

1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310
*      *      *      *      *      *      *      *
AGCAGTGGAC TTAATCGGTT GACCCTACTG TGGATTGGTG GGTTCGGGGG TGAAGCAAGT
TCGTCACCTG AATTAGCCAA CTGGGATGAC ACCTAACCAC CCAAAGCCCC ACTTCGTTCA

1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370
*      *      *      *      *      *      *      *
TCACTACAGC ATCAATAGAA AGTCATCTTT GAGATAATTT AACCCTGCCT CTCAGAGGGT
AGTGATGTCG TAGTTATCTT TCAGTAGAAA CTCTATTAAA TTGGGACGGA GAGTCTCCCA

1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430
*      *      *      *      *      *      *      *
TTTCTCTCCC AATTTTCTTT TTAATCCCCC TCTTAAGGGG GCCTTGAAT CTATAGTATA
AAAGAGAGGG TTAAGAGAAA AATGAGGGGG AGAATTCCCC CGGAACCTTA GATATCATAT

1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490
*      *      *      *      *      *      *      *
GAATGAACCTG TCTAGATGGA TGAATTATGA TAAAGGCTTA GGAATTCAAA AGGTGATTAA
CTTACTTGAC AGATCTACCT ACTTAATACT ATTTCCGAAT CCTGAAGTTT TCCACTAATT

1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550
*      *      *      *      *      *      *      *
ATATTTTAATG ATGTGTCATA TGAGTCCTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
TATAAATTAC TACACAGTAT ACTCAGGAGT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

1555 1560 1565 1570 1575 1580 1585 1590 1595 1600
*      *      *      *      *      *      *      *
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA (SEQ ID NO:3)
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TT

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FIG. 6

5	10	15	20	25	30	35	40	45	50	55
	*		*		*		*		*	
CTAGGGTCCC CGGCGCCAGG CCACCCGGCC GTCAGCAGC ATG CAG GGT AAA CGC AAA										
GATCCCAGGG GCCGCGGTCC GGTGGGCCGG CAGTCGTCG TAC GTC CCA TTT GCG TTT										
Met Gln Gly Lys Arg Lys>										
60	65	70	75	80	85	90	95	100	105	
*		*		*		*		*		
GCA CTG AAG TTG AAT TTT GCA AAT CCA CCT TTC AAA TCT ACA GCA AGG										
CGT GAC TTC AAC TTA AAA CGT TTA GGT GGA AAG TTT AGA TGT CGT TCC										
Ala Leu Lys Leu Asn Phe Ala Asn Pro Pro Phe Lys Ser Thr Ala Arg>										
110	115	120	125	130	135	140	145	150		
*		*		*		*		*		
TTT ACT CTG AAT CCC AAT CCT ACA GGA GTT CAA AAC CCA CAC ATA GAG										
AAA TGA GAC TTA GGG TTA GGA TGT CCT CAA GTT TTG GGT GTG TAT CTC										
Phe Thr Leu Asn Pro Asn Pro Thr Gly Val Gln Asn Pro His Ile Glu>										
155	160	165	170	175	180	185	190	195	200	
	*		*		*		*		*	
AGA CTG AGA ACA CAC AGC ATT GAG TCA TCA GGA AAA CTG AAG ATC TCC										
TCT GAC TCT TGT GTG TCG TAA CTC AGT AGT CCT TTT GAC TTC TAG AGG										
Arg Leu Arg Thr His Ser Ile Glu Ser Ser Gly Lys Leu Lys Ile Ser>										
205	210	215	220	225	230	235	240	245		
	*		*		*		*			
CCT GAA CAA CAC TGG GAT TTC ACT GCA GAG GAC TTG AAA GAC CTT GGA										
GGA CTT GTT GTG ACC CTA AAG TGA CGT CTC CTG AAC TTT CTG GAA CCT										
Pro Glu Gln His Trp Asp Phe Thr Ala Glu Asp Leu Lys Asp Leu Gly>										
250	255	260	265	270	275	280	285	290	295	
*		*		*		*		*		
GAA ATT GGA CGA GGA GCT TAT GGT TCT GTC AAC AAA ATG GTC CAC AAA										
CTT TAA CCT GCT CCT CGA ATA CCA AGA CAG TTG TTT TAC CAG GTG TTT										
Glu Ile Gly Arg Gly Ala Tyr Gly Ser Val Asn Lys Met Val His Lys>										
300	305	310	315	320	325	330	335	340	345	
*		*		*		*		*		
CCA AGT GGG CAA ATA ATG GCA GTT AAA AGA ATT CGG TCA ACA GTG GAT										
GGT TCA CCC GTT TAT TAC CGT CAA TTT TCT TAA GCC AGT TGT CAC CTA										
Pro Ser Gly Gln Ile Met Ala Val Lys Arg Ile Arg Ser Thr Val Asp>										
350	355	360	365	370	375	380	385	390		
*		*		*		*		*		
GAA AAA GAA CAA AAA CAA CTT CTT ATG GAT TTG GAT GTA GTA ATG CGG										
CTT TTT CTT GTT TTT GTT GAA GAA TAC CTA AAC CTA CAT CAT TAC GCC										
Glu Lys Glu Gln Lys Gln Leu Leu Met Asp Leu Asp Val Val Met Arg>										
395	400	405	410	415	420	425	430	435	440	
	*		*		*		*		*	
AGT AGT GAT TGC CCA TAC ATT GTT CAG TTT TAT GGT GCA CTC TTC AGA										
TCA TCA CTA ACG GGT ATG TAA CAA GTC AAA ATA CCA CGT GAG AAG TCT										
Ser Ser Asp Cys Pro Tyr Ile Val Gln Phe Tyr Gly Ala Leu Phe Arg>										
445	450	455	460	465	470	475	480	485		
	*		*		*		*			
GAG GGT GAC TGT TGG ATC TGT ATG GAA CTC ATG TCT ACC TCG TTT GAT										
CTC CCA CTG ACA ACC TAG ACA TAC CTT GAG TAC AGA TGG AGC AAA CTA										
Glu Gly Asp Cys Trp Ile Cys Met Glu Leu Met Ser Thr Ser Phe Asp>										

[illegible]

490	495	500	505	510	515	520	525	530	535						
AAG	TTT	TAC	AAA	TAT	GTA	TAT	AGT	GTA	TTA	GAT	GAT	GTT	ATT	CCA	GAA
TTC	AAA	ATG	TTT	ATA	CAT	ATA	TCA	CAT	AAT	CTA	CTA	CAA	TAA	GGT	CTT
Lys	Phe	Tyr	Lys	Tyr	Val	Tyr	Ser	Val	Leu	Asp	Asp	Val	Ile	Pro	Glu
540	545	550	555	560	565	570	575	580	585						
GAA	ATT	TTA	GGC	AAA	ATC	ACT	TTA	GCA	ACT	GTG	AAA	GCA	CTA	AAC	CAC
CTT	TAA	AAT	CCG	TTT	TAG	TGA	AAT	CGT	TGA	CAC	TTT	CGT	GAT	TTG	GTG
Glu	Ile	Leu	Gly	Lys	Ile	Thr	Leu	Ala	Thr	Val	Lys	Ala	Leu	Asn	His
590	595	600	605	610	615	620	625	630							
TTA	AAA	GAA	AAC	TTG	AAA	ATT	ATT	CAC	AGA	GAT	ATC	AAA	CCT	TCC	AAT
AAT	TTT	CTT	TTG	AAC	TTT	TAA	TAA	GTG	TCT	CTA	TAG	TTT	GGG	AGG	TTA
Leu	Lys	Glu	Asn	Leu	Lys	Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn
635	640	645	650	655	660	665	670	675	680						
ATT	CTT	CTG	GAC	AGA	AGT	GGA	AAT	ATT	AAG	CTC	TGT	GAC	TTC	GGC	ATC
TAA	GAA	GAC	CTG	TCT	TCA	CCT	TTA	TAA	TTC	GAG	ACA	CTG	AAG	CCG	TAG
Ile	Leu	Leu	Asp	Arg	Ser	Gly	Asn	Ile	Lys	Leu	Cys	Asp	Phe	Gly	Ile
685	690	695	700	705	710	715	720	725							
AGT	GGA	CAG	CTT	GTG	GAC	TCT	ATT	GCC	AAG	ACA	AGA	GAT	GCT	GGC	TGT
TCA	CCT	GTC	GAA	CAC	CTG	AGA	TAA	CGG	TTC	TGT	TCT	CTA	CGA	CCG	ACA
Ser	Gly	Gln	Leu	Val	Asp	Ser	Ile	Ala	Lys	Thr	Arg	Asp	Ala	Gly	Cys
730	735	740	745	750	755	760	765	770	775						
AGG	CCA	TAC	ATG	GCA	CCT	GAA	AGA	ATA	GAC	CCA	AGC	GCA	TCA	CGA	CAA
TCC	GGT	ATG	TAC	CGT	GGA	CTT	TCT	TAT	CTG	GGT	TCG	CGT	AGT	GCT	GTT
Arg	Pro	Tyr	Met	Ala	Pro	Glu	Arg	Ile	Asp	Pro	Ser	Ala	Ser	Arg	Gln
780	785	790	795	800	805	810	815	820	825						
GGA	TAT	GAT	GTC	CGC	TCT	GAT	GTC	TGG	AGT	TTG	GGG	ATC	ACA	TTG	TAT
CCT	ATA	CTA	CAG	GCG	AGA	CTA	CAG	ACC	TCA	AAC	CCC	TAG	TGT	AAC	ATA
Gly	Tyr	Asp	Val	Arg	Ser	Asp	Val	Trp	Ser	Leu	Gly	Ile	Thr	Leu	Tyr
830	835	840	845	850	855	860	865	870							
GAG	TTG	GCC	ACA	GGC	CGA	TTT	CCT	TAT	CCA	AAG	TGG	AAT	AGT	GTA	TTT
CTC	AAC	CGG	TGT	CCG	GCT	AAA	GGA	ATA	GGT	TTC	ACC	TTA	TCA	CAT	AAA
Glu	Leu	Ala	Thr	Gly	Arg	Phe	Pro	Tyr	Pro	Lys	Trp	Asn	Ser	Val	Phe
875	880	885	890	895	900	905	910	915	920						
GAT	CAA	CTA	ACA	CAA	GTC	GTG	AAA	GGA	GAT	CCT	CCG	CAG	CTG	AGT	AAT
CTA	GTT	GAT	TGT	GTT	CAG	CAC	TTT	CCT	CTA	GGA	GGC	GTC	GAC	TCA	TTA
Asp	Gln	Leu	Thr	Gln	Val	Val	Lys	Gly	Asp	Pro	Pro	Gln	Leu	Ser	Asn
925	930	935	940	945	950	955	960	965							
TCT	GAG	GAA	AGG	GAA	TTC	TCC	CCG	AGT	TTC	ATC	AAC	TTT	GTC	AAC	TTG
AGA	CTC	CTT	TCC	CTT	AAG	AGG	GGC	TCA	AAG	TAG	TTG	AAA	CAG	TTG	AAC
Ser	Glu	Glu	Arg	Glu	Phe	Ser	Pro	Ser	Phe	Ile	Asn	Phe	Val	Asn	Leu
970	975														

FIG. 6 - CONT'D

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TGC CTT ACG AAG GAT GAA TCC AAA AGG CCA AAG TAT AAA GAG CTT CTG
ACG GAA TGC TTC CTA CTT AGG TTT TCC GGT TTC ATA TTT CTC GAA GAC
Cys Leu Thr Lys Asp Glu Ser Lys Arg Pro Lys Tyr Lys Glu Leu Leu>

1020 1025 1030 1035 1040 1045 1050 1055 1060 1065
* * * * *
AAA CAT CCC TTT ATT TTG ATG TAT GAA GAA CGT GCC GTT GAG GTC GCA
TTT GTA GGG AAA TAA AAC TAC ATA CTT CTT GCA CGG CAA CTC CAG CGT
Lys His Pro Phe Ile Leu Met Tyr Glu Glu Arg Ala Val Glu Val Ala>

1070 1075 1080 1085 1090 1095 1100 1105 1110
* * * * *
TGC TAT GTT TGT AAA ATC CTG GAT CAA ATG CCA GCT ACT CCC AGC TCT
ACG ATA CAA ACA TTT TAG GAC CTA GTT TAC GGT CGA TGA GGG TCG AGA
Cys Tyr Val Cys Lys Ile Leu Asp Gln Met Pro Ala Thr Pro Ser Ser>

1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170
* * * * *
CCC ATG TAT GTC GAT TG ATATCGYTGC TACATCAGAC TCTAGAAAAA AGGGCTGAGA
GGG TAC ATA CAG CTA AC TATAGCRACG ATGTAGTCTG AGATCTTTTT TCCCAGACTCT
Pro Met Tyr Val Asp> (SEQ ID NO:6)

1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230
* * * * *
GGAAGCAAGA CGTAAAGAAT TTTTCATCCCG TATCACAGTG TTTTATTGTC TCGCCAGAC
CCTTCGTTCT GCATTTCTTA AAAGTAGGGC ATAGTGTAC CAAAAATAACG AGCGGGTCTG

1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290
* * * * *
ACCATGTGCA ATAAGATTGG TGTTTCGTTTC CATCATGTCT GTATACTCCT GTCACCTAGA
TGGTACACGT TATTCTAACC ACAAGCAAAG GTAGTACAGA CATATGAGGA CAGTGGATCT

1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350
* * * * *
ACGTGCATCC TTGTAATACC TGATTGATCA CACAGTGTTA GTGCTGGTCA GAGAGACCTC
TGCACGTAGG AACATTATGG ACTAACTAGT GTGTCACAAT CACGACCAGT CTCTCTGGAG

1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410
* * * * *
ATCCTGCTCT TTTGTGATGA ACATATTTCAT GAAATGTGGA AGTCAGTACG ATCAAGTTGT
TAGGACGAGA AAACACTACT TGTATAAGTA CTTTACACCT TCAGTCATGC TAGTTCAACA

1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470
* * * * *
TGA CTGTGAT TAGATCACAT CTAAATTCA TTTCTAGACT CAAAACCTGG AGATGCAGCT
ACTGACACTA ATCTAGTGTA GAATTTAAGT AAAGATCTGA GTTTTGGACC TCTACGTCGA

1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530
* * * * *
ACTGGAATGG TGTTTTGTCA GACTTCCAAA TCCTGGAAGG ACACAGTGAT GAATGTACTA
TGACCTTACC ACAAACAGT CTGAAGGTTT AGGACCTTCC TGTGTCACTA CTTACATGAT

1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590
* * * * *
TATCTGAACA TAGAACTCG GGCTTGAGTG AGAAGAGCTT GCACAGCCAA CGAGACACAT
ATAGACTTGT ATCTTTGAGC CCGAACTCAC TCTTCTCGAA CGTGTCGGTT GCTCTGTGTA

1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650
* * * * *
TGCCTTCTGG AGCTGGGAGA CAAAGGAGGA ATTTACTTTC TTCACCAAGT GCAATAGATT
ACGGAAGACC TCGACCCTCT GTTTCCTCCT TAAATGAAAG AAGTGGTCA CGTTATCTAA

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FIG. 6 - CONT'D

1655 1660	1665 1670	1675 1680	1685 1690	1695 1700	1705 1710
ACTGATGTGA	TATTCCTGTTG	CTTTACAGTT	ACAGTTGATG	TTTGGGGATC	GATGTGCTCA
TGACTACACT	ATAAGACAAC	GAAATGTCAA	TGTCAACTAC	AAACCCCTAG	CTACACGAGT
1715 1720	1725 1730	1735 1740	1745 1750	1755 1760	1765 1770
GCCAAATTTT	CTGTTTGAAA	TATCATGTTA	AATTAGAATG	AATTTATCTT	TACCAAAAAC
CGGTTTAAAG	GACAAACTTT	ATAGTACAAT	TTAATCTTAC	TTAAATAGAA	ATGGTTTTTG
1775 1780	1785 1790	1795 1800	1805 1810	1815 1820	1825 1830
CATGTTGCGT	TCAAAGAGGT	GAACATTAAA	ATATAGAGAC	AGGACAGAAT	GTGTTCTTTT
GTACAACGCA	AGTTTCTCCA	CTTGTAATTT	TATATCTCTG	TCCTGTCTTA	CACAAGAAAA
1835 1840	1845 1850	1855 1860	1865 1870	1875 1880	1885 1890
CTCCTCTACC	AGTCCTATTT	TTCAATGGGA	AGACTCAGGA	GTCTGCCACT	TGTCAAAGAA
GAGGAGATGG	TCAGGATAAA	AAGTTACCCCT	TCTGAGTCCT	CAGACGGTGA	ACAGTTTCTT
1895 1900	1905 1910	1915 1920	1925 1930	1935 1940	1945 1950
GGTGCTGATC	CTAAGAATTT	TTCAATCTCA	GAATTCGGTG	TGCTGCCAAC	TTGATGTTCC
CCACGACTAG	GATTCTTAAA	AAGTAAGAGT	CTTAAGCCAC	ACGACGGTTG	AACTACAAGG
1955 1960	1965 1970	1975 1980	1985 1990	1995 2000	2005 2010
ACCTGCCACA	AACCACCAGG	ACTGAAAGAA	GAAAACAGTA	CAGAAGGCCAA	AGTTTACAGA
TGGACGGTGT	TTGGTGGTCC	TGACTTTCTT	CTTTTGTCAT	GTCTTCCGTT	TCAAATGTCT
2015 2020	2025 2030	2035 2040	2045 2050	2055 2060	2065 2070
TGTTTTTAAT	TCTAGTATTT	TATCTGGAAC	AACTTGTAGC	AGCTATATAT	TTCCCTTGG
ACAAAAATTA	AGATCATAAA	ATAGACCTTG	TTGAACATCG	TCGATATATA	AAGGGGAACC
2075 2080	2085 2090	2095 2100	2105 2110	2115 2120	2125 2130
TCCCAAGCCT	GATACTTTAG	CCATCATAAC	TCACCTAACAG	GGAGAAGTAG	CTAGTAGCAA
AGGGTTCCGA	CTATGAAATC	GGTAGTATTG	AGTGATTGTC	CCTCTTCATC	GATCATCGTT
2135 2140	2145 2150	2155 2160	2165 2170	2175 2180	2185 2190
TGTGCCTTGA	TTGATTAGAT	AAAGATTTCT	AGTAGGCAGC	AAAAGACCAA	ATCTCAGTTG
ACACGGAAC	AACTAATCTA	TTTCTAAAGA	TCATCCGTCG	TTTTCTGGTT	TAGAGTCAAC
2195 2200	2205 2210	2215 2220	2225 2230	2235 2240	2245 2250
TTTGCTTCTT	GCCATCACTG	GTCCAGGTCT	TCAGTTTCCG	AATCTCTTTT	CCTTCCCCTG
AAACGAAGAA	CGGTAGTGAC	CAGGTCCAGA	AGTCAAAGGC	TTAGAGAAAG	GGAAGGGGAC
2255 2260	2265 2270	2275 2280	2285 2290	2295 2300	2305 2310
TGGTCTATTG	TCGCTATGTG	ACTTGCGCTT	AATCCAATAT	TTTGCTTTTT	TTCTATATCA
ACCAGATAAC	AGCGATACAC	TGAACGCGAA	TTAGGTTATA	AAACGGAAAA	AAGATATAGT
2315 2320	2325 2330	2335 2340	2345 2350	2355 2360	2365 2370
AAAAACCTTT	ACAGTTAGCA	GGGATGTTCC	TTACCGAGGA	TTTTTAACCC	CCAATCTCTC
TTTTTTGAAA	TGTCAATCGT	CCCTACAAGG	AATGGCTCCT	AAAAATTGGG	GGTTAGAGAG
2375 2380	2385 2390	2395 2400	2405 2410	2415 2420	2425 2430

FIG. 6 - CONT'D

ATAATCGCTA	GTGTTTAAAA	GGCTAAGAAT	AGTGGGGCCC	AACCGATGTG	GTAGGTGATA
TATTAGCGAT	CACAAATTTT	CCGATTCTTA	TCACCCCGGG	TTGGCTACAC	CATCCACTAT
2435 2440	2445 2450	2455 2460	2465 2470	2475 2480	2485 2490
*	*	*	*	*	*
AAGAGGCATC	TTTTCTAGAG	ACACATTGGA	CCAGATGAGG	ATCCGAAACG	GCAGCCTTTA
TTCTCCGTAG	AAAAGATCTC	TGTGTAACCT	GGTCTACTCC	TAGGCTTTGC	CGTCGGAAAT
2495 2500	2505 2510	2515 2520	2525 2530	2535 2540	2545 2550
*	*	*	*	*	*
CGTTCATCAC	CTGCTAGAAC	CTCTCGTAGT	CCATCACCAT	TTCTTGCCAT	TGGAATTCTA
GCAAGTAGTG	GACGATCTTG	GAGAGCATCA	GGTAGTGGTA	AAGAACCGTA	ACCTTAAGAT
2555 2560	2565 2570	2575 2580	2585 2590	2595 2600	2605 2610
*	*	*	*	*	*
CTGGAAAAAA	ATACAAAAAG	CAAAACAAAA	CCCTCAGCAC	TGTTACAAGA	GGCCATTTAA
GACCTTTTTT	TATGTTTTTC	GTTTTGTTTT	GGGAGTCGTG	ACAATGTTCT	CCGGTAAATT
2615 2620	2625 2630	2635 2640	2645 2650	2655 2660	2665 2670
*	*	*	*	*	*
GTATCTTG TG	CTTCTTCACT	TACCCATTAG	CCAGGTTCTC	ATTAGGTTTT	GCTTGGGCCT
CATAGAACAC	GAAGAAGTGA	ATGGGTAATC	GGTCCAAGAG	TAATCCAAAA	CGAACCCGGA
2675 2680	2685 2690	2695 2700	2705 2710	2715 2720	2725 2730
*	*	*	*	*	*
CCCTGGCACT	GAACCTTAGG	CTTTGTATGA	CAGTGAAGCA	GCACTGTGAG	TGGTTCAAGC
GGGACCGTGA	CTTGGAATCC	GAAACATACT	GTCACTTCGT	CGTGACACTC	ACCAAGTTCC
2735 2740	2745 2750	2755 2760	2765 2770	2775 2780	2785 2790
*	*	*	*	*	*
ACACTGGAAT	ATAAAACAGT	CATGGCCTGA	GATGCAGGTG	ATGCCATTAC	AGAACCAAAT
TGTGACCTTA	TATTTTGTCA	GTACCGGACT	CTACGTCCAC	TACGGTAATG	TCTTGGTTTA
2795 2800	2805 2810	2815 2820	2825 2830	2835 2840	2845 2850
*	*	*	*	*	*
CGTGGCACGT	ATTGCTGTGT	CTCCTCTCAG	AGTGACAGTC	ATAAATACTG	TCAAACAATA
GCACCGTGCA	TAACGACACA	GAGGAGAGTC	TCACTGTCAG	TATTTATGAC	AGTTTGTAT
2855 2860	2865 2870	2875 2880	2885 2890	2895 2900	2905 2910
*	*	*	*	*	*
AAGGGAGAAAT	GGTGCTGTTT	AAAGTCACAT	CCCTGTAAAT	TGCAGAATTC	AAAAGTGATT
TTCCCTCTTA	CCACGACAAA	TTTCAGTGTA	GGGACATTTA	ACGTCTTAAG	TTTTCACTAA
2915 2920	2925 2930	2935 2940	2945 2950	2955 2960	2965 2970
*	*	*	*	*	*
ATCTCTTTGA	TCTACTTGCC	TCATTTCCCT	ATCTTCTCCC	CCACGGTATC	CTAAACTTTA
TAGAGAAACT	AGATGAACGG	AGTAAAGGGA	TAGAAGAGGG	GGTGCCATAG	GATTTGAAAT
2975 2980	2985 2990	2995 3000	3005 3010	3015 3020	3025 3030
*	*	*	*	*	*
GACTTCCCAC	TGTTCTGAAA	GGAGACATTG	CTCTATGTCT	GCCTTCGACC	ACAGCAAGCC
CTGAAGGGTG	ACAAGACTTT	CCTCTGTAAC	GAGATACAGA	CGGAAGCTGG	TGTCGTTCCG
3035 3040	3045 3050	3055 3060	3065 3070	3075 3080	3085 3090
*	*	*	*	*	*
ATCATCCTCC	ATTGCTCCCG	GGGACTCAAG	AGGAATCTGT	TTCTCTGCTG	TCAACTTCCC
TAGTAGGAGG	TAACGAGGGC	CCCTGAGTTC	TCCTTAGACA	AAGAGACGAC	AGTTGAAGGG
3095 3100	3105 3110	3115 3120	3125 3130	3135 3140	3145 3150
*	*	*	*	*	*
ATCTGGCTCA	GCATAGGGTC	ACTTTGCCAT	TATGCAAATG	GAGATAAAAG	CAATTCTGGC
TAGACCGAGT	CGTATCCAG	TGAAACGGTA	ATACGTTTAC	CTCTATTTTC	GTTAAGACCG

FIG. 6 - CONT'D

3155 3160	3165 3170	3175 3180	3185 3190	3195 3200	3205 3210
* *	* *	* *	* *	* *	* *
TGTCCAGGAG	CTAATCTGAC	CGTTCTATTG	TGTGGATGAC	CACATAAGAA	GGCAATTTTA
ACAGGTCCTC	GATTAGACTG	GCAAGATAAC	ACACCCTACTG	GTGTATTCTT	CCGTTAAAAAT
3215 3220	3225 3230	3235 3240	3245 3250	3255 3260	3265 3270
* *	* *	* *	* *	* *	* *
GTGTATTAAT	CATAGATTAT	TATAAACTAT	AAACTTAAGG	GCAAGGAGTT	TATTACAATG
CACATAATTA	GTATCTAATA	ATATTTGATA	TTTGAATTCC	CGTTCCTCAA	ATAATGTTAC
3275 3280	3285 3290	3295 3300	3305 3310	3315 3320	3325 3330
* *	* *	* *	* *	* *	* *
TATCTTTTATT	AAAACAAAAG	GGTGTATAGT	GTTCACAAAC	TGTGAAAATA	GTGTAAGAAC
ATAGAAATAA	TTTTGTTTTT	CCACATATCA	CAAGTGTTTG	ACACTTTTAT	CACATTCCTG
3335 3340	3345 3350	3355 3360	3365 3370	3375 3380	3385 3390
* *	* *	* *	* *	* *	* *
TGTACATTGT	GAGCTCTGGT	TATTTTTCTC	TTGTACCATA	GAAAAATGTA	TAAAAATTAT
ACATGTAACA	CTCGAGACCA	ATAAAAAAGAG	AACATGGTAT	CTTTTTACAT	ATTTTTAATA
3395 3400	3405 3410	3415 3420	3425 3430	3435 3440	3445 3450
* *	* *	* *	* *	* *	* *
CAAAAAGCTA	ATGTGCAGGG	ATATTGCCTT	ATTTGTCTGT	AAAAAATGGA	GCTCAGTAAC
GTTTTTTCGAT	TACACGTCCC	TATAACGGAA	TAAACAGACA	TTTTTTACCT	CGAGTCATTG
3455 3460	3465 3470	3475 3480	3485 3490	3495	
* *	* *	* *	* *		
ATAACTGCTT	CTTGGAGCTT	TGGAATATTT	TATCCTGTAT	TCTTGTTT	(SEQ ID NO:5)
TATTGACGAA	GAACCTCGAA	ACCTTATAAA	ATAGGACATA	AGAACAAA	

FIG. 7

5	10	15	20	25	30	35	40	45	50
	*		*		*		*		*
CAACA	ATG	GCG	GCT	CCG	AGC	CCG	AGC	GGT	GGC
GGT	GGC	GGC	GGC	GGC	AGC	GGC	ACC	CCC	
Met	Ala	Ala	Pro	Ser	Pro	Ser	Gly	Gly	Gly
55	60	65	70	75	80	85	90	95	
	*		*		*		*		
GGC	CCC	GTA	GGG	TCC	CCG	GCG	CCA	GGC	CAC
CCG	GGG	CAT	CCC	AGG	GGC	CGC	GGT	CCG	GTG
Gly	Pro	Val	Gly	Ser	Pro	Ala	Pro	Gly	His
100	105	110	115	120	125	130	135	140	145
*		*		*		*		*	
CAG	GGT	AAA	CGC	AAA	GCA	CTG	AAG	TTG	AAT
GTC	CCA	TTT	GCG	TTT	CGT	GAC	TTC	AAC	TTA
Gln	Gly	Lys	Arg	Lys	Ala	Leu	Lys	Leu	Asn
150	155	160	165	170	175	180	185	190	
*		*		*		*		*	
AAA	TCT	ACA	GCA	AGG	TTT	ACT	CTG	AAT	CCC
TTT	AGA	TGT	CGT	TCC	AAA	TGA	GAC	TTA	GGG
Lys	Ser	Thr	Ala	Arg	Phe	Thr	Leu	Asn	Pro
195	200	205	210	215	220	225	230	235	240
*		*		*		*		*	
AAC	CCA	CAC	ATA	GAG	AGA	CTG	AGA	ACA	CAC
TTG	GGT	GTG	TAT	CTC	TCT	GAC	TCT	TGT	GTG
Asn	Pro	His	Ile	Glu	Arg	Leu	Arg	Thr	His
245	250	255	260	265	270	275	280	285	290
*		*		*		*		*	
AAA	CTG	AAG	ATC	TCC	CCT	GAA	CAA	CAC	TGG
TTT	GAC	TTC	TAG	AGG	GGA	CTT	GTT	GTG	ACC
Lys	Leu	Lys	Ile	Ser	Pro	Glu	Gln	His	Trp
295	300	305	310	315	320	325	330	335	
*		*		*		*		*	
TTG	AAA	GAC	CTT	GGA	GAA	ATT	GGA	CGA	GGA
AAC	TTT	CTG	GAA	CCT	CTT	TAA	CCT	GCT	CGA
Leu	Lys	Asp	Leu	Gly	Glu	Ile	Gly	Arg	Gly
340	345	350	355	360	365	370	375	380	385
*		*		*		*		*	
AAA	ATG	GTC	CAC	AAA	CCA	AGT	GGG	CAA	ATA
TTT	TAC	CAG	GTG	TTT	GGT	TCA	CCC	GTT	TAT
Lys	Met	Val	His	Lys	Pro	Ser	Gly	Gln	Ile
390	395	400	405	410	415	420	425	430	
*		*		*		*		*	
CGG	TCA	ACA	GTG	GAT	GAA	AAA	GAA	CAA	AAA
GCC	AGT	TGT	CAC	CTA	CTT	TTT	CTT	GTT	TTT
Arg	Ser	Thr	Val	Asp	Glu	Lys	Glu	Gln	Lys
435	440	445	450	455	460	465	470	475	480
*		*		*		*		*	
GAT	GTA	GTA	ATG	CGG	AGT	AGT	GAT	TGC	CCA
CTA	CAT	CAT	TAC	GCC	TCA	TCA	CTA	ACG	GGT
Asp	Val	Val	Met	Arg	Ser	Ser	Asp	Cys	Pro

FIG. 7 - CONT'D

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485      490      495      500      505      510      515      520      525      530
      *              *              *              *
GGT GCA CTC TTC AGA GAG GGT GAC TGT TGG ATC TGT ATG GAA CTC ATG
CCA CGT GAG AAG TCT CTC CCA CTG ACA ACC TAG ACA TAC CTT GAG TAC
Gly Ala Leu Phe Arg Glu Gly Asp Cys Trp Ile Cys Met Glu Leu Met>

535      540      545      550      555      560      565      570      575
      *              *              *              *
TCT ACC TCG TTT GAT AAG TTT TAC AAA TAT GTA TAT AGT GTA TTA GAT
AGA TGG AGC AAA CTA TTC AAA ATG TTT ATA CAT ATA TCA CAT AAT CTA
Ser Thr Ser Phe Asp Lys Phe Tyr Lys Tyr Val Tyr Ser Val Leu Asp>

580      585      590      595      600      605      610      615      620      625
      *              *              *              *
GAT GTT ATT CCA GAA GAA ATT TTA GGC AAA ATC ACT TTA GCA ACT GTG
CTA CAA TAA GGT CTT CTT TAA AAT CCG TTT TAG TGA AAT CGT TGA CAC
Asp Val Ile Pro Glu Glu Ile Leu Gly Lys Ile Thr Leu Ala Thr Val>

630      635      640      645      650      655      660      665      670
      *              *              *              *
AAA GCA CTA AAC CAC TTA AAA GAA AAC TTG AAA ATT ATT CAC AGA GAT
TTT CGT GAT TTG GTG AAT TTT CTT TTG AAC TTT TAA TAA GTG TCT CTA>
Lys Ala Leu Asn His Leu Lys Glu Asn Leu Lys Ile Ile His Arg Asp>

675      680      685      690      695      700      705      710      715      720
      *              *              *              *
ATC AAA CCT TCC AAT ATT CTT CTG GAC AGA AGT GGA AAT ATT AAG CTC
TAG TTT GGA AGG TTA TAA GAA GAC CTG TCT TCA CCT TTA TAA TTC GAG
Ile Lys Pro Ser Asn Ile Leu Leu Asp Arg Ser Gly Asn Ile Lys Leu>

725      730      735      740      745      750      755      760      765      770
      *              *              *              *
TGT GAC TTC GGC ATC AGT GGA CAG CTT GTG GAC TCT ATT GCC AAG ACA
ACA CTG AAG CCG TAG TCA CCT GTC GAA CAC CTG AGA TAA CGG TTC TGT
Cys Asp Phe Gly Ile Ser Gly Gln Leu Val Asp Ser Ile Ala Lys Thr>

775      780      785      790      795      800      805      810      815
      *              *              *              *
AGA GAT GCT GGC TGT AGG CCA TAC ATG GCA CCT GAA AGA ATA GAC CCA
TCT CTA CGA CCG ACA TCC GGT ATG TAC CGT GGA CTT TCT TAT CTG GGT
Arg Asp Ala Gly Cys Arg Pro Tyr Met Ala Pro Glu Arg Ile Asp Pro>

820      825      830      835      840      845      850      855      860      865
      *              *              *              *
AGC GCA TCA CGA CAA GGA TAT GAT GTC CGC TCT GAT GTC TGG AGT TTG
TCG CGT AGT GCT GTT CCT ATA CTA CAG GCG AGA CTA CAG ACC TCA AAC
Ser Ala Ser Arg Gln Gly Tyr Asp Val Arg Ser Asp Val Trp Ser Leu>

870      875      880      885      890      895      900      905      910
      *              *              *              *
GGG ATC ACA TTG TAT GAG TTG GCC ACA GGC CGA TTT CCT TAT CCA AAG
CCC TAG TGT AAC ATA CTC AAC CGG TGT CCG GCT AAA GGA ATA GGT TTC
Gly Ile Thr Leu Tyr Glu Leu Ala Thr Gly Arg Phe Pro Tyr Pro Lys>

915      920      925      930      935      940      945      950      955      960
      *              *              *              *
TGG AAT AGT GTA TTT GAT CAA CTA ACA CAA GTC GTG AAA GGA GAT CCT
ACC TTA TCA CAT AAA CTA GTT GAT TGT GTT CAG CAC TTT CCT CTA GGA
Trp Asn Ser Val Phe Asp Gln Leu Thr Gln Val Val Lys Gly Asp Pro>

965      970      975      980      985      990      995      1000      1005      1010
      *              *              *              *

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FIG. 7 - CONT'D

CGG CAG CTG AGT AAT TCT GAG GAA AGG GAA TTC TCC CCG AGT TTC ATC
 GGC GTC GAC TCA TTA AGA CTC CTT TCC CTT AAG AGG GGC TCA AAG TAG
 Pro Gln Leu Ser Asn Ser Glu Glu Arg Glu Phe Ser Pro Ser Phe Ile>

1015 1020 1025 1030 1035 1040 1045 1050 1055
 * * * * *
 AAC TTT GTC AAC TTG TGC CTT ACG AAG GAT GAA TCC AAA AGG CCA AAG
 TTG AAA CAG TTG AAC ACG GAA TGC TTC CTA CTT AGG TTT TCC GGT TTC
 Asn Phe Val Asn Leu Cys Leu Thr Lys Asp Glu Ser Lys Arg Pro Lys>

1060 1065 1070 1075 1080 1085 1090 1095 1100 1105
 * * * * *
 TAT AAA GAG CTT CTG AAA CAT CCC TTT ATT TTG ATG TAT GAA GAA CGT
 ATA TTT CTC GAA GAC TTT GTA GGG AAA TAA AAC TAC ATA CTT CTT GCA
 Tyr Lys Glu Leu Leu Lys His Pro Phe Ile Leu Met Tyr Glu Glu Arg>

1110 1115 1120 1125 1130 1135 1140 1145 1150
 * * * * *
 GCC GTT GAG GTC GCA TGC TAT GTT TGT AAA ATC CTG GAT CAA ATG CCA
 CGG CAA CTC CAG CGT ACG ATA CAA ACA TTT TAG GAC CTA GTT TAC GGT
 Ala Val Glu Val Ala Cys Tyr Val Cys Lys Ile Leu Asp Gln Met Pro>

1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
 * * * * *
 GCT ACT CCC AGC TCT CCC ATG TAT GTC GAT TGATAT CGYTGCTACA
 CGA TGA GGG TCG AGA GGG TAC ATA CAG CTA ACTATA GCRACGATGT
 Ala Thr Pro Ser Ser Pro Met Tyr Val Asp> (SEQ ID NO:8)

1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260
 * * * * *
 TCAGACTCTA GAAAAAAGGG CTGAGAGGAA GCAAGACGTA AAGAATTTTC ATCCCGTATC
 AGTCTGAGAT CTTTTTTCCC GACTCTCCTT CGTTCTGCAT TTCTTAAAG TAGGGCATAG

1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320
 * * * * *
 ACA GTGTTTT TATTGCTCGC CCAGACACCA TGTGCAATAA GATTGGTGTT CGTTTCCATC
 TGTCAAAAA ATAACGAGCG GGTCTGTGGT ACACGTTATT CTAACCACAA GCAAAGGTAG

1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380
 * * * * *
 ATGTCTGTAT ACTCCTGTCA CCTAGAACGT GCATCCTTGT AATACCTGAT TGATCACACA
 TACAGACATA TGAGGACAGT GGATCTTGCA CGTAGGAACA TTATGGACTA ACTAGTGTGT

1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440
 * * * * *
 GTGTTAGTGC TGGTCAGAGA GACCTCATCC TGCTCTTTTG TGATGAACAT ATTCATGAAA
 CACAATCAG ACCAGTCTCT CTGGAGTAGG ACGAGAAAAC ACTACTTGTA TAAGTACTTT

1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500
 * * * * *
 TGTGGAAGTC AGTACGATCA AGTTGTTGAC TGTGATTAGA TCACATCTTA AATTCATTTT
 ACACCTTCAG TCATGCTAGT TCAACAACCTG AACTAATCT AGTGTAGAAT TTAAGTAAAG

1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560
 * * * * *
 TAGACTCAAA ACCTGGAGAT GCAGCTACTG GAATGGTGTT TTGTCAGACT TCCAAATCCT
 ATCTGAGTTT TGGACCTCTA CGTCGATGAC CTTACCACAA AACAGTCTGA AGGTTTAGGA

1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620
 * * * * *
 GGAAGGACAC AGTGATGAAT GTACTATATC TGAACATAGA AACTCGGGCT TGAGTGAGAA
 CCTTCCTGTG TCACTACTTA CATGATATAG ACTTGTATCT TTGAGCCCGA ACTCACTCTT

FIG. 7 - CONT'D

1625 1630	1635 1640	1645 1650	1655 1660	1665 1670	1675 1680
* *	* *	* *	* *	* *	* *
GAGCTTGAC	AGCCAACGAG	ACACATTGCC	TTCTGGAGCT	GGGAGACAAA	GGAGGAATTT
CTCGAACGTG	TCGGTTGCTC	TGTGTAACGG	AAGACCTCGA	CCCTCTGTTT	CCTCCTTAAA
1685 1690	1695 1700	1705 1710	1715 1720	1725 1730	1735 1740
* *	* *	* *	* *	* *	* *
ACTTTCTTCA	CCAAGTGCAA	TAGATTACTG	ATGTGATATT	CTGTTGCTTT	ACAGTTACAG
TGAAAGAAGT	GGTTCACGTT	ATCTAATGAC	TACACTATAA	GACAACGAAA	TGTCAATGTC
1745 1750	1755 1760	1765 1770	1775 1780	1785 1790	1795 1800
* *	* *	* *	* *	* *	* *
TTGATGTTTG	GGGATCGATG	TGCTCAGCCA	AATTTCTCTG	TTGAAATATC	ATGTTAAATT
AACTACAAAC	CCCTAGCTAC	ACGAGTCGGT	TTAAAGGACA	AACTTTTATAG	TACAATTTAA
1805 1810	1815 1820	1825 1830	1835 1840	1845 1850	1855 1860
* *	* *	* *	* *	* *	* *
AGAATGAATT	TATCTTTACC	AAAAACCATG	TTGCGTTCAA	AGAGGTGAAC	ATTAAAAATAT
TCTTACTTAA	ATAGAAATGG	TTTTTGGTAC	AACGCAAGTT	TCTCCACTTG	TAATTTTATA
1865 1870	1875 1880	1885 1890	1895 1900	1905 1910	1915 1920
* *	* *	* *	* *	* *	* *
AGAGACAGGA	CAGAAATGTT	TCTTTTCTCC	TCTACCAGTC	CTATTTTTTCA	ATGGGAAGAC
TCTCTGTCCT	GTCTTACACA	AGAAAAGAGG	AGATGGTCAG	GATAAAAAGT	TACCCCTCTG
1925 1930	1935 1940	1945 1950	1955 1960	1965 1970	1975 1980
* *	* *	* *	* *	* *	* *
TCAGGAGTCT	GCCACTTGTC	AAAGAAGGTG	CTGATCCTAA	GAATTTTTTCA	TTCTCAGAAT
AGTCCTCAGA	CGGTGAACAG	TTTCTTCCAC	GACTAGGATT	CTTAAAAAGT	AAGAGTCTTA
1985 1990	1995 2000	2005 2010	2015 2020	2025 2030	2035 2040
* *	* *	* *	* *	* *	* *
TCGGTGTGCT	GCCAACTTGA	TGTTCCACCT	GCCACAAACC	ACCAGGACTG	AAAGAAGAAA
AGCCACACGA	CGGTTGAACT	ACAAGGTGGA	CGGTGTTTGG	TGGTCCTGAC	TTTCTTCTTT
2045 2050	2055 2060	2065 2070	2075 2080	2085 2090	2095 2100
* *	* *	* *	* *	* *	* *
ACAGTACAGA	AGGCAAAGTT	TACAGATGTT	TTTAATTCTA	GTATTTTATC	TGGAACAACT
TGTCATGTCT	TCCGTTTCAA	ATGTCTACAA	AAATTAAGAT	CATAAAATAG	ACCTTGTTGA
2105 2110	2115 2120	2125 2130	2135 2140	2145 2150	2155 2160
* *	* *	* *	* *	* *	* *
TGTAGCAGCT	ATATATTTCC	CCTTGGTCCC	AAGCCTGATA	CTTTAGCCAT	CATAACTCAC
ACATCGTCTG	TATATAAAGG	GGAACCAGGG	TTCCGACTAT	GAAATCGGTA	GTATTGAGTG
2165 2170	2175 2180	2185 2190	2195 2200	2205 2210	2215 2220
* *	* *	* *	* *	* *	* *
TAACAGGGAG	AAGTAGCTAG	TAGCAATGTG	CCTTGATTGA	TTAGATAAAG	ATTCTAGTA
ATTGTCCCTC	TTCATCGATC	ATCGTTACAC	GGAACCTAAT	AATCTATTTT	TAAAGATCAT
2225 2230	2235 2240	2245 2250	2255 2260	2265 2270	2275 2280
* *	* *	* *	* *	* *	* *
GGCAGCAAAA	GACCAAATCT	CAGTTGTTTG	CTTCTTGCCA	TCACTGGTCC	AGGTCTTCAG
CCGTCGTTTT	CTGGTTTAGA	GTCAACAAAC	GAAGAACGGT	AGTGACCAGG	TCCAGAAGTC
2285 2290	2295 2300	2305 2310	2315 2320	2325 2330	2335 2340
* *	* *	* *	* *	* *	* *
TTTCCGAATC	TCTTTCCCTT	CCCCTGTGGT	CTATTGTTCG	TATGTGACTT	GCGCTTAATC
AAAGGCTTAG	AGAAAGGGAA	GGGGACACCA	GATAACAGCG	ATACACTGAA	CGCCAATTAG
2345 2350	2355 2360	2365 2370	2375 2380	2385 2390	2395 2400

FIG. 7 - CONT'D

CAATATTTTG	CCTTTTTTCT	ATATCAAAAA	ACCTTTTACAG	TTAGCAGGGA	TGTTCCCTTAC
GTTATAAAAC	GGAAAAAAGA	TATAGTTTTT	TGGAAATGTC	AATCGTCCCT	ACAAGGAATG
2405 2410	2415 2420	2425 2430	2435 2440	2445 2450	2455 2460
CGAGGATTTT	TAACCCCCAA	TCTCTCATAA	TCGCTAGTGT	TTAAAAGGCT	AAGAATAGTG
GCTCCTAAAA	ATTGGGGGTT	AGAGAGTATT	AGCGATCACA	AATTTTCCGA	TTCTTATCAC
2465 2470	2475 2480	2485 2490	2495 2500	2505 2510	2515 2520
GGGCCCAACC	GATGTGGTAG	GTGATAAAGA	GGCATCTTTT	CTAGAGACAC	ATTGGACCAG
CCCGGGTTGG	CTACACCATC	CACTATTTC	CCGTAGAAAA	GATCTCTGTG	TAACCTGGTC
2525 2530	2535 2540	2545 2550	2555 2560	2565 2570	2575 2580
ATGAGGATCC	GAAACGGCAG	CCTTTACGTT	CATCACCTGC	TAGAACCTCT	CGTAGTCCAT
TACTCCTAGG	CTTTGCCGTC	GGAAATGCAA	GTAGTGACG	ATCTTGAGA	GCATCAGGTA
2585 2590	2595 2600	2605 2610	2615 2620	2625 2630	2635 2640
CACCATTTCT	TGGCATTTGA	ATTCTACTGG	AAAAAAATAC	AAAAAGCAAA	ACAAAACCTT
GTGGTAAAGA	ACCGTAACCT	TAAGATGACC	TTTTTTTATG	TTTTTCGTTT	TGTTTTGGGA
2645 2650	2655 2660	2665 2670	2675 2680	2685 2690	2695 2700
CAGCACTGTT	ACAAGAGGCC	ATTTAAGTAT	CTTGTGCTTC	TTCACCTACC	CATTAGCCAG
GTCGTGACAA	TGTTCTCCGG	TAAATTCATA	GAACACGAAG	AAGTGAATGG	GTAATCGGTC
2705 2710	2715 2720	2725 2730	2735 2740	2745 2750	2755 2760
GTTCTCATTA	GGTTTTGCTT	GGGCTCCCT	GGCACTGAAC	CTTAGGCTTT	GTATGACAGT
CAAGAGTAAT	CCAAAACGAA	CCCGGAGGGA	CCGTGACTTG	GAATCCGAAA	CATACTGTCA
2765 2770	2775 2780	2785 2790	2795 2800	2805 2810	2815 2820
GAAGCAGCAC	TGTGAGTGGT	TCAAGCACAC	TGGAATATAA	AACAGTCATG	GCCTGAGATG
CTTCGTCTGT	ACACTCACCA	AGTTCGTGTG	ACCTTATATT	TTGTCAGTAC	CGGACTCTAC
2825 2830	2835 2840	2845 2850	2855 2860	2865 2870	2875 2880
CAGGTGATGC	CATTACAGAA	CCAAATCGTG	GCACGTATTG	CTGTGTCTCC	TCTCAGAGTG
GTCCACTACG	GTAATGTCTT	GGTTTAGCAC	CGTGCATAAC	GACACAGAGG	AGAGTCTCAC
2885 2890	2895 2900	2905 2910	2915 2920	2925 2930	2935 2940
ACAGTCATAA	ATACTGTCAA	ACAATAAAGG	GAGAATGGTG	CTGTTTAAAG	TCACATCCCT
TGTCAGTATT	TATGACAGTT	TGTTATTTC	CTCTTACCAC	GACAAATTTT	AGTGTAGGGA
2945 2950	2955 2960	2965 2970	2975 2980	2985 2990	2995 3000
GTAAATTGCA	GAATTCAAAA	GTGATTATCT	CTTTGATCTA	CTTGCCTCAT	TTCCCTATCT
CATTTAACGT	CTTAAGTTTT	CACTAATAGA	GAAACTAGAT	GAACGGAGTA	AAGGGATAGA
3005 3010	3015 3020	3025 3030	3035 3040	3045 3050	3055 3060
TCTCCCCCAC	GGTATCCTAA	ACTTTAGACT	TCCCCTGTT	CTGAAAGGAG	ACATTGCTCT
AGAGGGGGTG	CCATAGGATT	TGAAATCTGA	AGGGTGACAA	GACTTTTCCT	TGTAACGAGA
3065 3070	3075 3080	3085 3090	3095 3100	3105 3110	3115 3120
ATGTCTGCCT	TCGACCACAG	CAAGCCATCA	TCCTCCATTG	CTCCCGGGGA	CTCAAGAGGA

FIG. 7 - CONT'D

TAQAGACGGA	AGCTGGTGTG	GTTCGGTAGT	AGGAGGTAAC	GAGGGCCCCT	GAGTTCTCCT
3125 3130	3135 3140	3145 3150	3155 3160	3165 3170	3175 3180
ATCTGTTTCT	CTGCTGTCAA	CTTCCCATCT	GGCTCAGCAT	AGGGTCACTT	TGCCATTATG
TAGACAAAGA	GACGACAGTT	GAAGGGTAGA	CCGAGTCGTA	TCCCAGTGAA	ACGGTAATAC
3185 3190	3195 3200	3205 3210	3215 3220	3225 3230	3235 3240
CAAATGGAGA	TAAAAGCAAT	TCTGGCTGTC	CAGGAGCTAA	TCTGACCGTT	CTATTGTGTG
GTTTACCTCT	ATTTTCGTTA	AGACCGACAG	GTCCTCGATT	AGACTGGCAA	GATAACACAC
3245 3250	3255 3260	3265 3270	3275 3280	3285 3290	3295 3300
GATGACCACA	TAAGAAGGCA	ATTTTAGTGT	ATTAATCATA	GATTATTATA	AACTATAAAC
CTACTGGTGT	ATTCTTCCGT	TAAAATCACA	TAATTAGTAT	CTAATAATAT	TTGATAATTTG
3305 3310	3315 3320	3325 3330	3335 3340	3345 3350	3355 3360
TTAAGGGCAA	GGAGTTTATT	ACAATGTATC	TTTATTAAAA	CAAAAGGGTG	TATAGTGTTT
AATTCCCCTT	CCTCAAATAA	TGTTACATAG	AAATAATTTT	GTTTTCCCAC	ATATCACAAG
3365 3370	3375 3380	3385 3390	3395 3400	3405 3410	3415 3420
ACAAACTGTG	AAAATAGTGT	AAGAACTGTA	CATTGTGAGC	TCTGGTTATT	TTTCTCTTGT
TGTTTGACAC	TTTTATCACA	TTCTTGACAT	GTAACACTCG	AGACCAATAA	AAAGAGAACA
3425 3430	3435 3440	3445 3450	3455 3460	3465 3470	3475 3480
ACCATAGAAA	AATGTATAAA	AATTATCAAA	AAGCTAATGT	GCAGGGATAT	TGCCTTATTT
TGGTATCTTT	TTACATATTT	TTAATAGTTT	TTCGATTACA	CGTCCCTATA	ACGGAATAAA
3485 3490	3495 3500	3505 3510	3515 3520	3525 3530	3535 3540
GTCTGTAAAA	AATGGAGCTC	AGTAACATAA	CTGCTTCTTG	GAGCTTTGGA	ATATTTTATC
CAGACATTTT	TTACCTCGAG	TCATTGTATT	GACGAAGAAC	CTCGAAACCT	TATAAAATAG
3545 3550					
CTGTATTCTT	GTTT	(SEQ ID NO:7)			
GACATAAGAA	CAAA				

FIG. 8

5	10	15	20	25	30	35	40	45	50
CTCCCAACA	ATG	GCG	GCT	CCG	AGC	CCG	AGC	GGC	GGC
GAGGGTTGT	TAC	CGC	CGA	GGC	TCG	GGC	TCG	CCG	CCG
Met	Ala	Ala	Pro	Ser	Pro	Ser	Gly	Gly	Gly
55	60	65	70	75	80	85	90	95	
GGC	AGC	GGC	AGC	GGC	ACC	CCC	GGC	CCC	GTA
CCG	TCG	CCG	TCG	CCG	TGG	GGG	CCG	GGG	CAT
Gly	Ser	Gly	Ser	Gly	Thr	Pro	Gly	Pro	Val
100	105	110	115	120	125	130	135	140	145
CAC	CCG	GCC	GTC	AGC	AGC	ATG	CAG	GGT	AAA
GTG	GGC	CCG	CAG	TCG	TCG	TAC	GTC	CCA	TTT
His	Pro	Ala	Val	Ser	Ser	Met	Gln	Gly	Lys
150	155	160	165	170	175	180	185	190	195
AAT	TTT	GCA	AAT	CCA	CCT	TTC	AAA	TCT	ACA
TTA	AAA	CGT	TTA	GGT	GGA	AAG	TTT	AGA	TGT
Asn	Phe	Ala	Asn	Pro	Pro	Phe	Lys	Ser	Thr
200	205	210	215	220	225	230	235	240	
CCC	AAT	CCT	ACA	GGA	GTT	CAA	AAC	CCA	CAC
GGG	TTA	GGA	TGT	CCT	CAA	GTT	TTG	GGT	GTG
Pro	Asn	Pro	Thr	Gly	Val	Gln	Asn	Pro	His
245	250	255	260	265	270	275	280	285	290
CAC	AGC	ATT	GAG	TCA	TCA	GGA	AAA	CTG	AAG
GTG	TCG	TAA	CTC	AGT	AGT	CCT	TTT	GAC	TTC
His	Ser	Ile	Glu	Ser	Ser	Gly	Lys	Leu	Lys
295	300	305	310	315	320	325	330	335	
TGG	GAT	TTC	ACT	GCA	GAG	GAC	TTG	AAA	GAC
ACC	CTA	AAG	TGA	CGT	CTC	CTG	AAC	TTT	CTG
Trp	Asp	Phe	Thr	Ala	Glu	Asp	Leu	Lys	Asp
340	345	350	355	360	365	370	375	380	385
GGA	GCT	TAT	GGT	TCT	GTC	AAC	AAA	ATG	GTC
CCT	CGA	ATA	CCA	AGA	CAG	TTG	TTT	TAC	CAG
Gly	Ala	Tyr	Gly	Ser	Val	Asn	Lys	Met	Val
390	395	400	405	410	415	420	425	430	435
ATA	ATG	GCA	GTT	AAA	AGA	ATT	CGG	TCA	ACA
TAT	TAC	CGT	CAA	TTT	TCT	TAA	GCC	AGT	TGT
Ile	Met	Ala	Val	Lys	Arg	Ile	Arg	Ser	Thr
440	445	450	455	460	465	470	475	480	
AAA	CAA	CTT	CTT	ATG	GAT	TTG	GAT	GTA	GTA
TTT	GTT	GAA	GAA	TAC	CTA	AAC	CTA	CAT	CAT
Lys	Gln	Leu	Leu	Met	Asp	Leu	Asp	Val	Val

GGC GGC GGC GGC GGC TCC GGG GGC
 CCG TCG CCG TCG CCG TGG GGG CCG GGG CAT CCC AGG GGC CGC GGT CCG
 Gly Ser Gly Ser Gly Thr Pro Gly Pro Val Gly Ser Pro Ala Pro Gly>
 CAC CCG GCC GTC AGC AGC ATG CAG GGT AAA CGC AAA GCA CTG AAG TTG
 GTG GGC CCG CAG TCG TCG TAC GTC CCA TTT GCG TTT CGT GAC TTC AAC
 His Pro Ala Val Ser Ser Met Gln Gly Lys Arg Lys Ala Leu Lys Leu>
 AAT TTT GCA AAT CCA CCT TTC AAA TCT ACA GCA AGG TTT ACT CTG AAT
 TTA AAA CGT TTA GGT GGA AAG TTT AGA TGT CGT TCC AAA TGA GAC TTA
 Asn Phe Ala Asn Pro Pro Phe Lys Ser Thr Ala Arg Phe Thr Leu Asn>
 CCC AAT CCT ACA GGA GTT CAA AAC CCA CAC ATA GAG AGA CTG AGA ACA
 GGG TTA GGA TGT CCT CAA GTT TTG GGT GTG TAT CTC TCT GAC TCT TGT
 Pro Asn Pro Thr Gly Val Gln Asn Pro His Ile Glu Arg Leu Arg Thr>
 CAC AGC ATT GAG TCA TCA GGA AAA CTG AAG ATC TCC CCT GAA CAA CAC
 GTG TCG TAA CTC AGT AGT CCT TTT GAC TTC TAG AGG GGA CTT GTT GTG
 His Ser Ile Glu Ser Ser Gly Lys Leu Lys Ile Ser Pro Glu Gln His>
 TGG GAT TTC ACT GCA GAG GAC TTG AAA GAC CTT GGA GAA ATT GGA CGA
 ACC CTA AAG TGA CGT CTC CTG AAC TTT CTG GAA CCT CTT TAA CCT GCT
 Trp Asp Phe Thr Ala Glu Asp Leu Lys Asp Leu Gly Glu Ile Gly Arg>
 GGA GCT TAT GGT TCT GTC AAC AAA ATG GTC CAC AAA CCA AGT GGG CAA
 CCT CGA ATA CCA AGA CAG TTG TTT TAC CAG GTG TTT GGT TCA CCC GTT
 Gly Ala Tyr Gly Ser Val Asn Lys Met Val His Lys Pro Ser Gly Gln>
 ATA ATG GCA GTT AAA AGA ATT CGG TCA ACA GTG GAT GAA AAA GAA CAA
 TAT TAC CGT CAA TTT TCT TAA GCC AGT TGT CAC CTA CTT TTT CTT GTT
 Ile Met Ala Val Lys Arg Ile Arg Ser Thr Val Asp Glu Lys Glu Gln>
 AAA CAA CTT CTT ATG GAT TTG GAT GTA GTA ATG CGG AGT AGT GAT TGC
 TTT GTT GAA GAA TAC CTA AAC CTA CAT CAT TAC GCC TCA TCA CTA ACG
 Lys Gln Leu Leu Met Asp Leu Asp Val Val Met Arg Ser Ser Asp Cys>

FIG. 8 - CONT'D

485	490	495	500	505	510	515	520	525	530						
	*		*		*		*		*						
CCA	TAC	ATT	GTT	CAG	TTT	TAT	GGT	GCA	CTC	TTC	AGA	GAG	GGT	GAC	TGT
GGT	ATG	TAA	CAA	GTC	AAA	ATA	CCA	CGT	GAG	AAG	TCT	CTC	CCA	CTG	ACA
Pro	Tyr	Ile	Val	Gln	Phe	Tyr	Gly	Ala	Leu	Phe	Arg	Glu	Gly	Asp	Cys>
535	540	545	550	555	560	565	570	575							
	*		*		*		*								
TGG	ATC	TGT	ATG	GAA	CTC	ATG	TCT	ACC	TCG	TTT	GAT	AAG	TTT	TAC	AAA
ACC	TAG	ACA	TAC	CTT	GAG	TAC	AGA	TGG	AGC	AAA	CTA	TTC	AAA	ATG	TTT
Trp	Ile	Cys	Met	Glu	Leu	Met	Ser	Thr	Ser	Phe	Asp	Lys	Phe	Tyr	Lys>
580	585	590	595	600	605	610	615	620	625						
*		*		*		*		*							
TAT	GTA	TAT	AGT	GTA	TTA	GAT	GAT	GTT	ATT	CCA	GAA	GAA	ATT	TTA	GGC
ATA	CAT	ATA	TCA	CAT	AAT	CTA	CTA	CAA	TAA	GGT	CTT	CTT	TAA	AAT	CCG
Tyr	Val	Tyr	Ser	Val	Leu	Asp	Asp	Val	Ile	Pro	Glu	Glu	Ile	Leu	Gly>
630	635	640	645	650	655	660	665	670	675						
*		*		*		*		*							
AAA	ATC	ACT	TTA	GCA	ACT	GTG	AAA	GCA	CTA	AAC	CAC	TTA	AAA	GAA	AAC
TTT	TAG	TGA	AAT	CGT	TGA	CAC	TTT	CGT	GAT	TTG	GTG	AAT	TTT	CTT	TTG
Lys	Ile	Thr	Leu	Ala	Thr	Val	Lys	Ala	Leu	Asn	His	Leu	Lys	Glu	Asn>
680	685	690	695	700	705	710	715	720							
*		*		*		*		*							
TTG	AAA	ATT	ATT	CAC	AGA	GAT	ATC	AAA	CCT	TCC	AAT	ATT	CTT	CTG	GAC
AAC	TTT	TAA	TAA	GTG	TCT	CTA	TAG	TTT	GGA	AGG	TTA	TAA	GAA	GAC	CTG
Leu	Lys	Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Leu	Leu	Asp>
725	730	735	740	745	750	755	760	765	770						
	*		*		*		*		*						
AGA	AGT	GGA	AAT	ATT	AAG	CTC	TGT	GAC	TTC	GGC	ATC	AGT	GGA	CAG	CTT
TCT	TCA	CCT	TTA	TAA	TTC	GAG	ACA	CTG	AAG	CCG	TAG	TCA	CCT	GTC	GAA
Arg	Ser	Gly	Asn	Ile	Lys	Leu	Cys	Asp	Phe	Gly	Ile	Ser	Gly	Gln	Leu>
775	780	785	790	795	800	805	810	815							
	*		*		*		*								
GTG	GAC	TCT	ATT	GCC	AAG	ACA	AGA	GAT	GCT	GGC	TGT	AGG	CCA	TAC	ATG
CAC	CTG	AGA	TAA	CGG	TTC	TGT	TCT	CTA	CGA	CCG	ACA	TCC	GGT	ATG	TAC
Val	Asp	Ser	Ile	Ala	Lys	Thr	Arg	Asp	Ala	Gly	Cys	Arg	Pro	Tyr	Met>
820	825	830	835	840	845	850	855	860	865						
*		*		*		*		*							
GCA	CCT	GAA	AGA	ATA	GAC	CCA	AGC	GCA	TCA	CGA	CAA	GGA	TAT	GAT	GTC
CGT	GGA	CTT	TCT	TAT	CTG	GGT	TCG	CGT	AGT	GCT	GTT	CCT	ATA	CTA	CAG
Ala	Pro	Glu	Arg	Ile	Asp	Pro	Ser	Ala	Ser	Arg	Gln	Gly	Tyr	Asp	Val>
870	875	880	885	890	895	900	905	910	915						
*		*		*		*		*							
CGC	TCT	GAT	GTC	TGG	AGT	TTG	GGG	ATC	ACA	TTG	TAT	GAG	TTG	GCC	ACA
CGC	AGA	CTA	CAG	ACC	TCA	AAC	CCC	TAG	TGT	AAC	ATA	CTC	AAC	CGG	TGT
Arg	Ser	Asp	Val	Trp	Ser	Leu	Gly	Ile	Thr	Leu	Tyr	Glu	Leu	Ala	Thr>
920	925	930	935	940	945	950	955	960							
*		*		*		*		*							
GGC	CGA	TTT	CCT	TAT	CCA	AAG	TGG	AAT	AGT	GTA	TTT	GAT	CAA	CTA	ACA
CCG	GCT	AAA	GGA	ATA	GGT	TTC	ACC	TTA	TCA	CAT	AAA	CTA	GTT	GAT	TGT
Gly	Arg	Phe	Pro	Tyr	Pro	Lys	Trp	Asn	Ser	Val	Phe	Asp	Gln	Leu	Thr>
965	970	975	980	985	990	995	1000	1005	1010						
	*		*		*		*		*						

FIG. 8 - CONT'D

CAA GTC GTG AAA GGA GAT CCT CCG CAG CTG AGT AAT TCT GAG GAA AGG
 GTT CAG CAC TTT CCT CTA GGA GGC GTC GAC TCA TTA AGA CTC CTT TCC
 Gln Val Val Lys Gly Asp Pro Pro Gln Leu Ser Asn Ser Glu Glu Arg>

1015 1020 1025 1030 1035 1040 1045 1050 1055

GAA TTC TCC CCG AGT TTC ATC AAC TTT GTC AAC TTG TGC CTT ACG AAG
 CTT AAG AGG GGC TCA AAG TAG TTG AAA CAG TTG AAC ACG GAA TGC TTC
 Glu Phe Ser Pro Ser Phe Ile Asn Phe Val Asn Leu Cys Leu Thr Lys>

1060 1065 1070 1075 1080 1085 1090 1095 1100 1105

GAT GAA TCC AAA AGG CCA AAG TAT AAA GAG CTT CTG AAA CAT CCC TTT
 CTA CTT AGG TTT TCC GGT TTC ATA TTT CTC GAA GAC TTT GTA GGG AAA
 Asp Glu Ser Lys Arg Pro Lys Tyr Lys Glu Leu Leu Lys His Pro Phe>

1110 1115 1120 1125 1130 1135 1140 1145 1150 1155

ATT TTG ATG TAT GAA GAA CGT GCC GTT GAG GTC GCA TGC TAT GTT TGT
 TAA AAC TAC ATA CTT CTT GCA CGG CAA CTC CAG CGT ACG ATA CAA ACA
 Ile Leu Met Tyr Glu Glu Arg Ala Val Glu Val Ala Cys Tyr Val Cys>

1160 1165 1170 1175 1180 1185 1190 1195 1200

AAA ATC CTG GAT CAA ATG CCA GCT ACT CCC AGC TCT CCC ATG TAT GTC
 TTT TAG GAC CTA GTT TAC GGT CGA TGA GGG TCG AGA GGG TAC ATA CAG
 Lys Ile Leu Asp Gln Met Pro Ala Thr Pro Ser Ser Pro Met Tyr Val>

1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260

GAT TGAT ATCGCTGCTA CATCAGACTC TAGAAAAAAG GGCTGAGAGG AAGCAAGACG
 CTA ACTA TAGCGACGAT GTAGTCTGAG ATCTTTTTTC CCGACTCTCC TTCGTTCTGC
 Asp> (SEQ ID NO:10)

1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320

TAAAGAATTT TCATCCCGTA TCACAGTGTT TTTATTGCTC GCCCAGACAC CATGTGCAAT
 ATTTCTTAAA AGTAGGGCAT AGTGTCAAA AAATAACGAG CGGGTCTGTG GTACACGTTA

1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380

AAGATTGGTG TTCGTTTCCA TCATGTCTGT ATACTCCTGT CACCTAGAAC GTGCATCCTT
 TTCTAACCAC AAGCAAAGGT AGTACAGACA TATGAGGACA GTGGATCTTG CACGTAGGAA

1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440

GTAATACCTG ATTGATCACA CAGTGTTAGT GCTGGTCAGA GAGACCTCAT CCTGCTCTTT
 CATTTATGGAC TAACTAGTGT GTCACAATCA CGACCAGTCT CTCTGGAGTA GGACGAGAAA

1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500

TGTGATGAAC ATATTCATGA AATGTGGAAG TCAGTACGAT CAAGTTGTG ACTGTGATTA
 AACTACTTG TATAAGTACT TTACACCTTC AGTCATGCTA GTTCAACAAC TGACACTAAT

1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560

GATCACATCT TAAATTCATT TCTAGACTCA AAACCTGGAG ATGCAGCTAC TCGAATGGTG
 CTAGTGTAGA ATTTAAGTAA AGATCTGAGT TTTGGACCTC TACGTCGATG ACCTTACCAC

1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620

TTTTGTCAGA CTTCCAAATC CTGGAAGGAC ACAGTGATGA ATGTACTATA TCTGAACATA

FIG. 8 - CONT'D

AAAACAGTCT	GAAGGTTTAG	GACCTTCCTG	TGTCACTACT	TACATGATAT	AGACTTGTAT
1625 1630	1635 1640	1645 1650	1655 1660	1665 1670	1675 1680
*	*	*	*	*	*
GAAACTCGGG	CTTGAGTGAG	AAGAGCTTGC	ACAGCCAACG	AGACACATTG	CCTTCTGGAG
CTTTGAGCCC	GAAGTCACTC	TTCTCGAACG	TGTCGGTTGC	TCTGTGTAAC	GGAAGACCTC
1685 1690	1695 1700	1705 1710	1715 1720	1725 1730	1735 1740
*	*	*	*	*	*
CTGGGAGACA	AAGGAGGAAT	TTACTTTCTT	CACCAAGTGC	AATAGATTAC	TGATGTGATA
GACCCCTCTGT	TTCCCTCCTTA	AATGAAAGAA	GTGGTTTCACG	TTATCTAATG	ACTACACTAT
1745 1750	1755 1760	1765 1770	1775 1780	1785 1790	1795 1800
*	*	*	*	*	*
TTCTGTTGCT	TTACAGTTAC	AGTTGATGTT	TGGGGATCGA	TGTGCTCAGC	CAAATTTCTT
AAGACAACGA	AATGTCAATG	TCAACTACAA	ACCCCTAGCT	ACACGAGTCG	GTTTAAAGGA
1805 1810	1815 1820	1825 1830	1835 1840	1845 1850	1855 1860
*	*	*	*	*	*
GTTTGAAATA	TCATGTTAAA	TTAGAATGAA	TTTATCTTTA	CCAAAAACCA	TGTTGCGTTC
CAAACTTTTAT	AGTACAATTT	AATCTTTACTT	AAATAGAAAT	GGTTTTTGGT	ACAACGCAAG
1865 1870	1875 1880	1885 1890	1895 1900	1905 1910	1915 1920
*	*	*	*	*	*
AAAGAGGTGA	ACATTAAAAT	ATAGAGACAG	GACAGAAATGT	GTTCTTTTTCT	CCTCTACCAG
TTTCTCCACT	TGTAATTTTA	TATCTCTGTC	CTGTCTTACA	CAAGAAAAGA	GGAGATGGTC
1925 1930	1935 1940	1945 1950	1955 1960	1965 1970	1975 1980
*	*	*	*	*	*
TCCTATTTTT	CAATGGGAAG	ACTCAGGAGT	CTGCCACTTG	TCAAAGAAGG	TGCTGATCCT
AGGATAAAAA	GTTACCCCTT	TGAGTCCTCA	GACGGTGAAC	AGTTTCTTCC	ACGACTAGGA
1985 1990	1995 2000	2005 2010	2015 2020	2025 2030	2035 2040
*	*	*	*	*	*
AAGAATTTTT	CATTCTCAGA	ATTCCGGTGTG	CTGCCAACTT	GATGTTCCAC	CTGCCACAAA
TTCTTAAAAA	GTAAGAGTCT	TAAGCCACAC	GACGGTTGAA	CTACAAGGTG	GACGGTGTTC
2045 2050	2055 2060	2065 2070	2075 2080	2085 2090	2095 2100
*	*	*	*	*	*
CCACCAGGAC	TGAAAGAAGA	AAACAGTACA	GAAGGCAAAG	TTTACAGATG	TTTTTAATTTC
GGTGGTCCCTG	ACTTTCTTCT	TTTGTCATGT	CTTCCGTTTC	AAATGTCTAC	AAAAATTAAG
2105 2110	2115 2120	2125 2130	2135 2140	2145 2150	2155 2160
*	*	*	*	*	*
TAGTATTTTA	TCTGGAACAA	CTTGTAGCAG	CTATATATTT	CCCCTTGGTC	CCAAGCCTGA
ATCATAAAAT	AGACCTTGTT	GAACATCGTC	GATATATAAA	GGGGAACCAG	GGTTCCGACT
2165 2170	2175 2180	2185 2190	2195 2200	2205 2210	2215 2220
*	*	*	*	*	*
TACTTTAGCC	ATCATAACTC	ACTAACAGGG	AGAAGTAGCT	AGTAGCAATG	TGCCTTGATT
ATGAAATCGG	TAGTATTGAG	TGATTGTCCC	TCITCATCGA	TCATCGTTAC	ACGGAACATA
2225 2230	2235 2240	2245 2250	2255 2260	2265 2270	2275 2280
*	*	*	*	*	*
GATTAGATAA	AGATTTCTAG	TAGGCAGCAA	AAGACCAAAT	CTCAGTTGTT	TGCTTCTTGC
CTAATCTATT	TCTAAAGATC	ATCCGTCGTT	TTCTGGTTTA	GAGTCAACAA	ACGAAGAACG
2285 2290	2295 2300	2305 2310	2315 2320	2325 2330	2335 2340
*	*	*	*	*	*
CATCACTGGT	CCAGGTCTTC	AGTTTCCGAA	TCTCTTTCCC	TTCCCTGTGT	GTCTATTGTC
GTAGTGACCA	GGTCCAGAAG	TCAAAGGCTT	AGAGAAAGGG	AAGGGGACAC	CAGATAACAG

FIG. 8 - CONT'D

2345	2350	2355	2360	2365	2370	2375	2380	2385	2390	2395	2400
GCTATGTGAC	TTGCGCTTAA	TCCAATATTT	TGCCTTTTTT	CTATATCAAA	AAACCTTTAC						
CGATACACTG	AACGCGAATT	AGGTTATAAA	ACGGAAAAAA	GATATAGTTT	TTTGGAATG						
2405	2410	2415	2420	2425	2430	2435	2440	2445	2450	2455	2460
AGTTAGCAGG	GATGTTCTTT	ACCGAGGATT	TTTAACCCCC	AATCTCTCAT	AATCGCTAGT						
TCAATCGTCC	CTACAAGGAA	TGGCTCCTAA	AAATTGCGGG	TTAGAGAGTA	TTAGCGATCA						
2465	2470	2475	2480	2485	2490	2495	2500	2505	2510	2515	2520
GTTTTAAAAGG	CTAAGAATAG	TGGGGCCCAA	CCGATGTGGT	AGGTGATAAA	GAGGCATCTT						
CAAATTTTCC	GATTCCTTATC	ACCCCGGGTT	GGCTACACCA	TCCACTATTT	CTCCGTAGAA						
2525	2530	2535	2540	2545	2550	2555	2560	2565	2570	2575	2580
TTCTAGAGAC	ACATTGGACC	AGATGAGGAT	CCGAAACGGC	AGCCTTTACG	TTCATCACCT						
AAGATCTCTG	TGTAACCTGG	TCTACTCCTA	GGCTTTGCCG	TGGGAAATGC	AAGTAGTGGA						
2585	2590	2595	2600	2605	2610	2615	2620	2625	2630	2635	2640
GCTAGAACCT	CTCGTAGTCC	ATCACCATTT	CTTGGCATTG	GAATTCCTACT	GGAAAAAAT						
CGATCTTGGA	GAGCATCAGG	TAGTGGTAAA	GAACCGTAAC	CTTAAGATGA	CCTTTTTTTA						
2645	2650	2655	2660	2665	2670	2675	2680	2685	2690	2695	2700
ACAAAAAGCA	AAACAAACC	CTCAGCACTG	TTACAAGAGG	CCATTTAAGT	ATCTTGTCCT						
TGTTTTTCGT	TTTGTTCG	GAGTCGTGAC	AATGTTCTCC	GGTAAATCA	TAGAACACGA						
2705	2710	2715	2720	2725	2730	2735	2740	2745	2750	2755	2760
TCTTCACTTA	CCCATTAGCC	AGGTTCTCAT	TAGGTTTTGC	TTGGGCCTCC	CTGGCACTGA						
AGAAGTGAAT	GGGTAATCGG	TCCAAGAGTA	ATCCAAAACG	AACCCGGAGG	GACCGTGACT						
2765	2770	2775	2780	2785	2790	2795	2800	2805	2810	2815	2820
ACCTTAGGCT	TTGTATGACA	GTGAAGCAGC	ACTGTGAGTG	GTTCAAGCAC	ACTGGAATAT						
TGGAATCCGA	AACATACTGT	CACTTCGTCTG	TGACACTCAC	CAAGTTCGTG	TGACCTTATA						
2825	2830	2835	2840	2845	2850	2855	2860	2865	2870	2875	2880
AAAACAGTCA	TGGCCTGAGA	TGCAGGTGAT	GCCATTACAG	AACCAAATCG	TGGCACGTAT						
TTTTGTCACT	ACCGGACTCT	ACGTCCACTA	CGGTAATGTC	TTGGTTTAGC	ACCGTGCATA						
2885	2890	2895	2900	2905	2910	2915	2920	2925	2930	2935	2940
TGCTGTGTCT	CCTCTCAGAG	TGACAGTCAT	AAATACTGTC	AAACAATAAA	GGGAGAATGG						
ACGACACAGA	GGAGAGTCTC	ACTGTCAGTA	TTTATGACAG	TTTGTTATTT	CCCTCTTACC						
2945	2950	2955	2960	2965	2970	2975	2980	2985	2990	2995	3000
TGCTGTTTAA	AGTCACATCC	CTGTAAATTG	CAGAATTCAA	AAGTGATTAT	CTCTTTGATC						
ACGACAAATT	TCAGTGTAGG	GACATTTAAC	GTCTTAAGTT	TTCCTAATA	GAGAACTAG						
3005	3010	3015	3020	3025	3030	3035	3040	3045	3050	3055	3060
TACTTGCCCTC	ATTTCCCTAT	CTTCTCCCCC	ACGGTATCCT	AAACTTTAGA	CTTCCCACTG						
ATGAACGGAG	TAAAGGGATA	GAAGAGGGGG	TGCCATAGGA	TTTGAAATCT	GAAGGGTGAC						
3065	3070	3075	3080	3085	3090	3095	3100	3105	3110	3115	3120

FIG. 8 - CONT'D

TTCTGAAAGG	AGACATTGCT	CTATGTCTGC	CTTCGACCAC	AGCAAGCCAT	CATCCTCCAT
AAGACTTTCC	TCTGTAACGA	GATACAGACG	GAAGCTGGTG	TCGTTCCGTA	GTAGGAGGTA
3125 3130	3135 3140	3145 3150	3155 3160	3165 3170	3175 3180
*	*	*	*	*	*
TGCTCCCGGG	GACTCAAGAG	GAATCTGTTT	CTCTGCTGTC	AACTTCCCAT	CTGGCTCAGC
ACGAGGGCCC	CTGAGTTCTC	CTTAGACAAA	GAGACGACAG	TTGAAGGGTA	GACCGAGTCG
3185 3190	3195 3200	3205 3210	3215 3220	3225 3230	3235 3240
*	*	*	*	*	*
ATAGGGTCAC	TTTGCCATTA	TGCAAATGGA	GATAAAAGCA	ATTCTGGCTG	TCCAGGAGCT
TATCCAGTG	AAACGGTAAT	ACGTTTACCT	CTATTTTCGT	TAAGACCGAC	AGGTCCTCGA
3245 3250	3255 3260	3265 3270	3275 3280	3285 3290	3295 3300
*	*	*	*	*	*
AATCTGACCG	TTCTATTGTG	TGGATGACCA	CATAAGAAGG	CAATTTTAGT	GTATTAATCA
TTAGACTGGC	AAGATAACAC	ACCTACTGGT	GTATTCCTCC	GTAAAAATCA	CATAATTAGT
3305 3310	3315 3320	3325 3330	3335 3340	3345 3350	3355 3360
*	*	*	*	*	*
TAGATTATTA	TAAACTATAA	ACTTAAGGGC	AAGGAGTTTA	TTACAATGTA	TCTTTATTAA
ATCTAATAAT	ATTTGATATT	TGAATTCCCG	TTCCTCAAAT	AATGTTACAT	AGAAATAATT
3365 3370	3375 3380	3385 3390	3395 3400	3405 3410	3415 3420
*	*	*	*	*	*
AACAAAAGGG	TGTATAGTGT	TCACAAACTG	TGAAAATAGT	GTAAGAACTG	TACATTGTGA
TTGTTTTCCC	ACATATCACA	AGTGTTTGAC	ACTTTTATCA	CATTCTTGAC	ATGTAACACT
3425 3430	3435 3440	3445 3450	3455 3460	3465 3470	3475 3480
*	*	*	*	*	*
GCTCTGGTTA	TTTTTCTCTT	GTACCATAGA	AAAATGTATA	AAAATTATCA	AAAAGCTAAT
CGAGACCAAT	AAAAAGAGAA	CATGGTATCT	TTTTACATAT	TTTAAATAGT	TTTTCGATTA
3485 3490	3495 3500	3505 3510	3515 3520	3525 3530	3535 3540
*	*	*	*	*	*
GTGCAGGGAT	ATTGCCTTAT	TTGTCTGTAA	AAAATGGAGC	TCAGTAACAT	AACTGCTTCT
CACGTCCCTA	TAACGGAATA	AACAGACATT	TTTTACCTCG	AGTCATTGTA	TTGACGAAGA
3545 3550	3555 3560	3565 3570	3575		
*	*	*			
TGGAGCTTTG	GAATATTTTA	TCCTGTATTC	TTGTTT	(SEQ ID NO:9)	
ACCTCGAAAC	CTTATAAAAT	AGGACATAAG	AACAAA		